

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Verfahren zur Herstellung von mehrfach ungesättigten Fettsäuren in transgenen Organismen

<130> PF54756

<140> 20030601

<141> 2003-08-01

<160> 192

<170> PatentIn version 3.1

<210> 1

<211> 1266

<212> DNA

<213> Euglena gracilis

<220>

<221> CDS

<222> (1)..(1266)

<223> Delta-8-Desaturase

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tat	gat	gtg	tct	gcc	tgg	gtc	aat	ttc	cac	cct	ggt	ggt	gcg	gaa	att	96
Tyr	Asp	Val	Ser	Ala	Trp	Val	Asn	Phe	His	Pro	Gly	Gly	Ala	Glu	Ile	
			20				25						30			

ata	gag	aat	tac	caa	gga	agg	gat	gcc	act	gat	gcc	ttc	atg	gtt	atg	144
Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met	
		35					40					45				

cac	tct	caa	gaa	gcc	ttc	gac	aag	ctc	aag	cgc	atg	ccc	aaa	atc	aat	192
His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn	
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ccc	agt	tct	gag	ttg	cca	ccc	cag	gct	gca	gtg	aat	gaa	gct	caa	gag	240
Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu	
65				70				75						80		

gat	ttc	cgg	aag	ctc	cga	gaa	gag	ttg	atc	gca	act	ggc	atg	ttt	gat	288
Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp	
				85				90						95		

gcc	tcc	ccc	ctc	tgg	tac	tca	tac	aaa	atc	agc	acc	aca	ctg	ggc	ctt	336
Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu	
			100					105					110			

gga	gtg	ctg	ggt	tat	ttc	ctg	atg	gtt	cag	tat	cag	atg	tat	ttc	att	384
Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile	
		115				120						125				

ggg	gca	gtg	ttg	ctt	ggg	atg	cac	tat	caa	cag	atg	ggc	tgg	ctt	tct	432
Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser	
		130				135					140					

cat	gac	att	tgc	cac	cac	cag	act	ttc	aag	aac	cgg	aac	tgg	aac	aac	480
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 <213> Euglena gracilis

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Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
 100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
 115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
 130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
 145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
 165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
 180 185 190

Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
 195 200 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
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Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
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1 5 10 15																	
gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg	96																
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro																	
20 25 30																	

5

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg 35 40 45	144
acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu 50 55 60	192
agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly 65 70 75 80	240
gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln 85 90 95	288
tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys 100 105 110	336
gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu 115 120 125	384
agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp 130 135 140	432
gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met 145 150 155 160	480
ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu 165 170 175	528
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met 180 185 190	576
cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile 195 200 205	624
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala 210 215 220	672
ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe 225 230 235 240	720
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys 245 250 255	768
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<212> PRT

<213> Isochrysis galbana

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 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
 35 40 45
 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
 50 55 60
 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
 65 70 75 80
 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
 85 90 95
 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
 100 105 110
 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
 115 120 125
 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
 130 135 140
 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
 145 150 155 160
 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
 165 170 175
 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
 180 185 190
 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
 195 200 205
 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
 210 215 220
 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
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 Gln Leu

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 gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96
 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
 20 25 30
 ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
 35 40 45
 gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60
 ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
 65 70 75 80
 acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat 288
 Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
 85 90 95
 ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa 336
 Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
 100 105 110
 cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg 384
 Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
 115 120 125
 gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg 432
 Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
 130 135 140
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 Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
 145 150 155 160
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 Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
 165 170 175
 aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc 576
 Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
 180 185 190
 ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa 624
 Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
 195 200 205
 cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat 672
 His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
 210 215 220

agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp 225 230 235 240	720
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ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val 325 330 335	1008
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe 340 345 350	1056
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu 355 360 365	1104
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly 370 375 380	1152
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu 385 390 395 400	1200
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ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr 420 425 430	1296
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His 435 440 445	1344
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro 450 455 460	1392
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35 40 45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
 325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
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ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe 35 40 45	144
cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu 50 55 60	192
ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys 65 70 75 80	240
gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn 85 90 95	288
att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu 100 105 110	336
cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe 115 120 125	384
tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe 130 135 140	432
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ggt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His 165 170 175	528
cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val 180 185 190	576
gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His 195 200 205	624
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 Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg.
 275 280 285

aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg 912
 Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
 290 295 300

tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg 960
 Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
 305 310 315 320

ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta 1008
 Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
 325 330 335

gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac 1056
 Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
 340 345 350

atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg 1104
 Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
 355 360 365

aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag 1152
 Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
 370 375 380

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 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400

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 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296
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 <213> Ceratodon purpureus

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Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60

13

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
 100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
 115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
 130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
 145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
 165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
 245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
 260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
 275 280 285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
 290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
 305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
 325 330 335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Asn Gly Leu Pro Tyr
405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
435 440 445

<210> 9
<211> 1443
<212> DNA
<213> Physcomitrella patens

<220>
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<222> (1)..(1443)
<223> Delta-5-Desaturase

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Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu
1 5 10 15
ttg agg cta cga acg tcg aat tca aag ggt ccc gaa caa gag caa act 96
Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr
20 25 30
ttg aag aag tac acc ctt gaa gat gtc agc cgc cac aac acc cca gca 144
Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala
35 40 45
gat tgt tgg ttg gtg ata tgg ggc aaa gtc tac gat gtc aca agc tgg 192
Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp
50 55 60
att ccc aat cat ccg ggg ggc agt ctc atc cac gta aaa gca ggg cag 240
Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln
65 70 75 80
gat tcc act cag ctt ttc gat tcc tat cac ccc ctt tat gtc agg aaa 288
Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys
85 90 95
atg ctc gcg aag tac tgt att ggg gaa tta gta ccg tct gct ggt gat 336
Met Leu Ala Lys Tyr Cys Ile Gly Glu Leu Val Pro Ser Ala Gly Asp
100 105 110

15

gac aag ttt aag aaa gca act ctg gag tat gca gat gcc gaa aat gaa Asp Lys Phe Lys Lys Ala Thr Leu Glu Tyr Ala Asp Ala Glu Asn Glu 115 120 125	384
gat ttc tat ttg gtt gtg aag caa cga gtt gaa tct tat ttc aag agt Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser 130 135 140	432
aac aag ata aac ccc caa att cat cca cat atg atc ctg aag tca ttg Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu 145 150 155 160	480
ttc att ctt ggg gga tat ttc gcc agt tac tat tta gcg ttc ttc tgg Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp 165 170 175	528
tct tca agt gtc ctt gtt tct ttg ttt ttc gca ttg tgg atg ggg ttc Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe 180 185 190	576
ttc gca gcg gaa gtc ggc gtg tcg att caa cat gat gga aat cat ggt Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly 195 200 205	624
tca tac act aaa tgg cgt ggc ttt gga tat atc atg gga gcc tcc cta Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu 210 215 220	672
gat cta gtc gga gcc agt agc ttc atg tgg aga cag caa cac gtt gtg Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val 225 230 235 240	720
gga cat cac tcg ttt aca aat gtg gac aac tac gat cct gat att cgt Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg 245 250 255	768
gtg aaa gat cca gat gtc agg agg gtt gcg acc aca caa cca aga caa Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln 260 265 270	816
tgg tat cat gcg tat cag cat atc tac ctg gca gta tta tat gga act Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr 275 280 285	864
cta gct ctt aag agt att ttt cta gat gat ttc ctt gcg tac ttc aca Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr 290 295 300	912
gga tca att ggc cct gtc aag gtg gcg aaa atg acc ccc ctg gag ttc Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe 305 310 315 320	960
aac atc ttc ttt cag gga aag ctg cta tat gcg ttc tac atg ttc gtg Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val 325 330 335	1008
ttg cca tct gtg tac ggt gtt cac tcc gga gga act ttc ttg gca cta Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu 340 345 350	1056
tat gtg gct tct cag ctc att aca ggt tgg atg tta gct ttt ctt ttt Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe 355 360 365	1104
caa gta gca cat gtc gtg gat gat gtt gca ttt cct aca cca gaa ggt Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly 370 375 380	1152

16

ggg aag gtg aag gga gga tgg gct gca atg cag gtt gca aca act acg 1200
 Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
 385 390 395 400
 gat ttc agt cca cgc tca tgg ttc tgg ggt cat gtc tct gga gga tta 1248
 Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
 405 410 415
 aac aac caa att gag cat cat ctg ttt cca gga gtg tgc cat gtt cat 1296
 Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
 420 425 430
 tat cca gcc att cag cct att gtc gag aag acg tgc aag gaa ttc gat 1344
 Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
 435 440 445
 gtg cct tat gta gcc tac cca act ttt tgg act gcg ttg aga gcc cac 1392
 Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
 450 455 460
 ttt gcg cat ttg aaa aag gtt gga ttg aca gag ttt cgg ctc gat ggc 1440
 Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
 465 470 475 480
 tga 1443

<210> 10
 <211> 480
 <212> PRT
 <213> Physcomitrella patens

<400> 10

Met Ala Pro His Ser Ala Asp Thr Ala Gly Leu Val Pro Ser Asp Glu
 1 5 10 15
 Leu Arg Leu Arg Thr Ser Asn Ser Lys Gly Pro Glu Gln Glu Gln Thr
 20 25 30
 Leu Lys Lys Tyr Thr Leu Glu Asp Val Ser Arg His Asn Thr Pro Ala
 35 40 45
 Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp
 50 55 60
 Ile Pro Asn His Pro Gly Gly Ser Leu Ile His Val Lys Ala Gly Gln
 65 70 75 80
 Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys
 85 90 95
 Met Leu Ala Lys Tyr Cys Ile Gly Glu Leu Val Pro Ser Ala Gly Asp
 100 105 110
 Asp Lys Phe Lys Lys Ala Thr Leu Glu Tyr Ala Asp Ala Glu Asn Glu
 115 120 125
 Asp Phe Tyr Leu Val Val Lys Gln Arg Val Glu Ser Tyr Phe Lys Ser
 130 135 140

Asn Lys Ile Asn Pro Gln Ile His Pro His Met Ile Leu Lys Ser Leu
145 150 155 160

Phe Ile Leu Gly Gly Tyr Phe Ala Ser Tyr Tyr Leu Ala Phe Phe Trp
165 170 175

Ser Ser Ser Val Leu Val Ser Leu Phe Phe Ala Leu Trp Met Gly Phe
180 185 190

Phe Ala Ala Glu Val Gly Val Ser Ile Gln His Asp Gly Asn His Gly
195 200 205

Ser Tyr Thr Lys Trp Arg Gly Phe Gly Tyr Ile Met Gly Ala Ser Leu
210 215 220

Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val
225 230 235 240

Gly His His Ser Phe Thr Asn Val Asp Asn Tyr Asp Pro Asp Ile Arg
245 250 255

Val Lys Asp Pro Asp Val Arg Arg Val Ala Thr Thr Gln Pro Arg Gln
260 265 270

Trp Tyr His Ala Tyr Gln His Ile Tyr Leu Ala Val Leu Tyr Gly Thr
275 280 285

Leu Ala Leu Lys Ser Ile Phe Leu Asp Asp Phe Leu Ala Tyr Phe Thr
290 295 300

Gly Ser Ile Gly Pro Val Lys Val Ala Lys Met Thr Pro Leu Glu Phe
305 310 315 320

Asn Ile Phe Phe Gln Gly Lys Leu Leu Tyr Ala Phe Tyr Met Phe Val
325 330 335

Leu Pro Ser Val Tyr Gly Val His Ser Gly Gly Thr Phe Leu Ala Leu
340 345 350

Tyr Val Ala Ser Gln Leu Ile Thr Gly Trp Met Leu Ala Phe Leu Phe
355 360 365

Gln Val Ala His Val Val Asp Asp Val Ala Phe Pro Thr Pro Glu Gly
370 375 380

Gly Lys Val Lys Gly Gly Trp Ala Ala Met Gln Val Ala Thr Thr Thr
385 390 395 400

Asp Phe Ser Pro Arg Ser Trp Phe Trp Gly His Val Ser Gly Gly Leu
405 410 415

Asn Asn Gln Ile Glu His His Leu Phe Pro Gly Val Cys His Val His
420 425 430

Tyr Pro Ala Ile Gln Pro Ile Val Glu Lys Thr Cys Lys Glu Phe Asp
435 440 445

Val Pro Tyr Val Ala Tyr Pro Thr Phe Trp Thr Ala Leu Arg Ala His
450 455 460

Phe Ala His Leu Lys Lys Val Gly Leu Thr Glu Phe Arg Leu Asp Gly
465 470 475 480

<210> 11
<211> 1320
<212> DNA
<213> Thraustrochytrium

<220>
<221> CDS
<222> (1)..(1320)
<223>

<400> 11
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gag gcg aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg 96
Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
20 25 30
tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc 144
Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
35 40 45
ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag 192
Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
50 55 60
ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg 240
Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
65 70 75 80
aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag 288
Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
85 90 95
gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag 336
Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
100 105 110
ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac 384
Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
115 120 125
cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg 432
Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
130 135 140
tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc 480
Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly

145	150	155	160	
att gcg cag ggc cgc tgc ggc tgg gtc atg cac gag atg ggc cac ggg Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly 165 170 175				528
tcg ttc acg ggc gtc atc tgg ctc gac gac cgg atg tgc gag ttc ttc Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe 180 185 190				576
tac ggc gtc ggc tgc ggc atg agc ggg cac tac tgg aag aac cag cac Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His 195 200 205				624
agc aag cac cac gcc gcg ccc aac cgc ctc gag cac gat gtc gat ctc Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu 210 215 220				672
aac acg ctg ccc ctg gtc gcc ttt aac gag cgc gtc gtg cgc aag gtc Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val 225 230 235 240				720
aag ccg gga tcg ctg ctg gcg ctc tgg ctg cgc gtg cag gcg tac ctc Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu 245 250 255				768
ttt gcg ccc gtc tcg tgc ctg ctc atc ggc ctt ggc tgg acg ctc tac Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr 260 265 270				816
ctg cac ccg cgc tac atg ctg cgc acc aag cgg cac atg gag ttc gtc Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val 275 280 285				864
tgg atc ttc gcg cgc tac att ggc tgg ttc tcg ctc atg ggc gct ctc Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu 290 295 300				912
ggc tac tcg ccg ggc acc tcg gtc ggg atg tac ctg tgc tcg ttc ggc Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly 305 310 315 320				960
ctc ggc tgc att tac att ttc ctg cag ttc gcc gtc agc cac acg cac Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His 325 330 335				1008
ctg ccg gtg acc aac ccg gag gac cag ctg cac tgg ctc gag tac gcg Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala 340 345 350				1056
gcc gac cac acg gtg aac att agc acc aag tcc tgg ctc gtc acg tgg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp 355 360 365				1104
tgg atg tcg aac ctg aac ttt cag atc gag cac cac ctc ttc ccc acg Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr 370 375 380				1152
gcg ccg cag ttc cgc ttc aag gaa atc agt cct cgc gtc gag gcc ctc Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu 385 390 395 400				1200
ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala 405 410 415				1248
gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly 420 425 430 435 440 445				1296

420 425 430 1320

gcc gac acc aag aag cag gac tga
Ala Asp Thr Lys Lys Gln Asp
435

<210> 12
<211> 439
<212> PRT
<213> Thraustrochytrium

<400> 12

Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala
1 5 10 15

Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu
20 25 30

Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe
35 40 45

Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu
50 55 60

Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro
65 70 75 80

Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln
85 90 95

Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu
100 105 110

Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr
115 120 125

Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met
130 135 140

Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly
145 150 155 160

Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly
165 170 175

Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe
180 185 190

Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His
195 200 205

Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val Asp Leu
210 215 220

Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val Arg Lys Val
 225 230 235 240

Lys Pro Gly Ser Leu Leu Ala Leu Trp Leu Arg Val Gln Ala Tyr Leu
 245 250 255

Phe Ala Pro Val Ser Cys Leu Leu Ile Gly Leu Gly Trp Thr Leu Tyr
 260 265 270

Leu His Pro Arg Tyr Met Leu Arg Thr Lys Arg His Met Glu Phe Val
 275 280 285

Trp Ile Phe Ala Arg Tyr Ile Gly Trp Phe Ser Leu Met Gly Ala Leu
 290 295 300

Gly Tyr Ser Pro Gly Thr Ser Val Gly Met Tyr Leu Cys Ser Phe Gly
 305 310 315 320

Leu Gly Cys Ile Tyr Ile Phe Leu Gln Phe Ala Val Ser His Thr His
 325 330 335

Leu Pro Val Thr Asn Pro Glu Asp Gln Leu His Trp Leu Glu Tyr Ala
 340 345 350

Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp Leu Val Thr Trp
 355 360 365

Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
 370 375 380

Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu
 385 390 395 400

Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala
 405 410 415

Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly
 420 425 430

Ala Asp Thr Lys Lys Gln Asp
 435

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 <211> 1341
 <212> DNA
 <213> Mortierella alpina

<220>
 <221> CDS
 <222> (1)..(1341)
 <223> Delta-5-Desaturase

<400> 13
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 Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala
 1 5 10 15

cat aac acc aag gac gac cta ctc ttg gcc atc cgc ggc agg gtg tac 96
 His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr
 20 25 30

gat gtc aca aag ttc ttg agc cgc cat cct ggt gga gtg gac act ctc 144
 Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu
 35 40 45

ctg ctc gga gct ggc cga gat gtt act ccg gtc ttt gag atg tat cac 192
 Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His
 50 55 60

gcg ttt ggg gct gca gat gcc att atg aag aag tac tat gtc ggt aca 240
 Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr
 65 70 75 80

ctg gtc tcg aat gag ctg ccc atc ttc ccg gag cca acg gtg ttc cac 288
 Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His
 85 90 95

aaa acc atc aag acg aga gtc gag ggc tac ttt acg gat cgg aac att 336
 Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile
 100 105 110

gat ccc aag aat aga cca gag atc tgg gga cga tac gct ctt atc ttt 384
 Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe
 115 120 125

gga tcc ttg atc gct tcc tac tac gcg cag ctc ttt gtg cct ttc gtt 432
 Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val
 130 135 140

gtc gaa cgc aca tgg ctt cag gtg gtg ttt gca atc atc atg gga ttt 480
 Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe
 145 150 155 160

gcg tgc gca caa gtc gga ctc aac cct ctt cat gat gcg tct cac ttt 528
 Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe
 165 170 175

tca gtg acc cac aac ccc act gtc tgg aag att ctg gga gcc acg cac 576
 Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His
 180 185 190

gac ttt ttc aac gga gca tcg tac ctg gtg tgg atg tac caa cat atg 624
 Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met
 195 200 205

ctc ggc cat cac ccc tac acc aac att gct gga gca gat ccc gac gtg 672
 Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val
 210 215 220

tcg acg tct gag ccc gat gtt cgt cgt atc aag ccc aac caa aag tgg 720
 Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp
 225 230 235 240

ttt gtc aac cac atc aac cag cac atg ttt gtt cct ttc ctg tac gga 768
 Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly
 245 250 255

ctg ctg gcg ttc aag gtg cgc att cag gac atc aac att ttg tac ttt 816
 Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe

260	265	270	
gtc aag acc aat gac gct att cgt gtc aat ccc atc tcg aca tgg cac			864
Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His			
275	280	285	
act gtg atg ttc tgg ggc ggc aag gct ttc ttt gtc tgg tat cgc ctg			912
Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu			
290	295	300	
att gtt ccc ctg cag tat ctg ccc ctg ggc aag gtg ctg ctc ttg ttc			960
Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe			
305	310	315	320
acg gtc gcg gac atg gtg tcg tct tac tgg ctg gcg ctg acc ttc cag			1008
Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln			
325	330	335	
gcg aac cac gtt gtt gag gaa gtt cag tgg ccg ttg cct gac gag aac			1056
Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn			
340	345	350	
ggg atc atc caa aag gac tgg gca gct atg cag gtc gag act acg cag			1104
Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln			
355	360	365	
gat tac gca cac gat tcg cac ctc tgg acc agc atc act ggc agc ttg			1152
Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu			
370	375	380	
aac tac cag gct gtg cac cat ctg ttc ccc aac gtg tcg cag cac cat			1200
Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His			
385	390	395	400
tat ccc gat att ctg gcc atc atc aag aac acc tgc agc gag tac aag			1248
Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys			
405	410	415	
gtt cca tac ctt gtc aag gat acg ttt tgg caa gca ttt gct tca cat			1296
Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His			
420	425	430	
ttg gag cac ttg cgt gtt ctt gga ctc cgt ccc aag gaa gag tag			1341
Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu			
435	440	445	
<210> 14			
<211> 446			
<212> PRT			
<213> Mortierella alpina			
<400> 14			
Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala			
1	5	10	15
His Asn Thr Lys Asp Asp Leu Leu Leu Ala Ile Arg Gly Arg Val Tyr			
20	25	30	
Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Gly Val Asp Thr Leu			
35	40	45	
Leu Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His			
50	55	60	

Ala Phe Gly Ala Ala Asp Ala Ile Met Lys Lys Tyr Tyr Val Gly Thr
65 70 75 80

Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His
85 90 95

Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile
100 105 110

Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe
115 120 125

Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Pro Phe Val
130 135 140

Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Ile Met Gly Phe
145 150 155 160

Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe
165 170 175

Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His
180 185 190

Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met
195 200 205

Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val
210 215 220

Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp
225 230 235 240

Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly
245 250 255

Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe
260 265 270

Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His
275 280 285

Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu
290 295 300

Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe
305 310 315 320

Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln
325 330 335

Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn
 340 345 350

Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln
 355 360 365

Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu
 370 375 380

Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His
 385 390 395 400

Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys
 405 410 415

Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His
 420 425 430

Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu
 435 440 445

<210> 15
 <211> 1344
 <212> DNA
 <213> Caenorhabditis elegans

<220>
 <221> CDS
 <222> (1)..(1344)
 <223> Delta-5-Desaturase

<400> 15 48
 atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
 1 5 10 15
 gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
 20 25 30
 ggt agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45
 cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60
 ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240
 Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
 65 70 75 80
 gat gac cca atc aaa gga att gat gat gtg aac atg gga act ttc aat 288
 Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
 85 90 95
 att tct gag aaa cga tct gcc caa ata aat aaa agt ttc act gat cta 336
 Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu

100	105	110	
cgt atg cga gtt cgt gca gaa gga ctt atg gat gga tct cct ttg ttc Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe 115 120 125			384
tac att aga aaa att ctt gaa aca atc ttc aca att ctt ttt gca ttc Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe 130 135 140			432
tac ctt caa tac cac aca tat tat ctt cca tca gct att cta atg gga Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly 145 150 155 160			480
gtt gcg tgg caa caa ttg gga tgg tta atc cat gaa ttc gca cat cat Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His 165 170 175			528
cag ttg ttc aaa aac aga tac tac aat gat ttg gcc agc tat ttc gtt Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val 180 185 190			576
gga aac ttt tta caa gga ttc tca tct ggt ggt tgg aaa gag cag cac Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His 195 200 205			624
aat gtg cat cac gca gcc aca aat gtt gtt gga cga gac gga gat ctt Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu 210 215 220			672
gat tta gtc cca ttc tat gct aca gtg gca gaa cat ctc aac aat tat Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr 225 230 235 240			720
tct cag gat tca tgg gtt atg act cta ttc aga tgg caa cat gtt cat Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His 245 250 255			768
tgg aca ttc atg tta cca ttc ctc cgt ctc tcg tgg ctt ctt cag tca Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser 260 265 270			816
atc att ttt gtt agt cag atg cca act cat tat tat gac tat tac aga Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg 275 280 285			864
aat act gcg att tat gaa cag gtt ggt ctc tct ttg cac tgg gct tgg Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp 290 295 300			912
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met 305 310 315 320			960
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val 325 330 335			1008
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn 340 345 350			1056
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met 355 360 365			1104
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			1152

370 375 380

att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act 1200
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400

gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac 1248
 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc 1296
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430

cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag 1344
 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 16
 <211> 447
 <212> PRT
 <213> Caenorhabditis elegans

<400> 16

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 1 5 10 15

Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
 20 25 30

Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
 35 40 45

His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
 50 55 60

Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
 65 70 75 80

Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
 85 90 95

Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
 100 105 110

Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
 115 120 125

Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
 130 135 140

Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
 145 150 155 160

Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
 165 170 175

Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
 180 185 190

Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
 195 200 205

Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
 210 215 220

Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
 225 230 235 240

Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
 245 250 255

Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
 260 265 270

Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
 275 280 285

Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
 290 295 300

Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
 305 310 315 320

Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
 325 330 335

Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
 340 345 350

Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
 355 360 365

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
 370 375 380

Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
 385 390 395 400

Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
 405 410 415

Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
 420 425 430

Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
 435 440 445

<210> 17
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 <212> DNA
 <213> Borago officinalis

<220>
 <221> CDS
 <222> (42)..(1388)
 <223> Delta-6-Desaturase

<400> 17
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 Met Ala Ala Gln Ile
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aag aaa tac att acc tca gat gaa ctc aag aac cac gat aaa ccc gga 104
 Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn His Asp Lys Pro Gly
 10 15 20

gat cta tgg atc tcg att caa ggg aaa gcc tat gat gtt tcg gat tgg 152
 Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr Asp Val Ser Asp Trp
 25 30 35

gtg aaa gac cat cca ggt ggc agc ttt ccc ttg aag agt ctt gct ggt 200
 Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu Lys Ser Leu Ala Gly
 40 45 50

caa gag gta act gat gca ttt gtt gca ttc cat cct gcc tct aca tgg 248
 Gln Glu Val Thr Asp Ala Phe Val Ala Phe His Pro Ala Ser Thr Trp
 55 60 65

aag aat ctt gat aag ttt ttc act ggg tat tat ctt aaa gat tac tct 296
 Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr Leu Lys Asp Tyr Ser
 70 75 80 85

gtt tct gag gtt tct aaa gat tat agg aag ctt gtg ttt gag ttt tct 344
 Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu Val Phe Glu Phe Ser
 90 95 100

aaa atg ggt ttg tat gac aaa aaa ggt cat att atg ttt gca act ttg 392
 Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile Met Phe Ala Thr Leu
 105 110 115

tgc ttt ata gca atg ctg ttt gct atg agt gtt tat ggg gtt ttg ttt 440
 Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val Tyr Gly Val Leu Phe
 120 125 130

tgt gag ggt gtt ttg gta cat ttg ttt tct ggg tgt ttg atg ggg ttt 488
 Cys Glu Gly Val Leu Val His Leu Phe Ser Gly Cys Leu Met Gly Phe
 135 140 145

ctt tgg att cag agt ggt tgg att gga cat gat gct ggg cat tat atg 536
 Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp Ala Gly His Tyr Met
 150 155 160 165

gta gtg tct gat tca agg ctt aat aag ttt atg ggt att ttt gct gca 584
 Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met Gly Ile Phe Ala Ala
 170 175 180

aat tgt ctt tca gga ata agt att ggt tgg tgg aaa tgg aac cat aat 632
 Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp Lys Trp Asn His Asn
 185 190 195

gca cat cac att gcc tgt aat agc ctt gaa tat gac cct gat tta caa 680
 Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr Asp Pro Asp Leu Gln

200	205	210	
tat ata cca ttc ctt gtt gtg tct tcc aag ttt ttt ggt tca ctc acc Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe Phe Gly Ser Leu Thr 215 220 225			728
tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe 230 235 240 245			776
ttt gta agt tat caa cat tgg aca ttt tac cct att atg tgt gct gct Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro Ile Met Cys Ala Ala 250 255 260			824
agg ctc aat atg tat gta caa tct ctc ata atg ttg ttg acc aag aga Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met Leu Leu Thr Lys Arg 265 270 275			872
aat gtg tcc tat cga gct cag gaa ctc ttg gga tgc cta gtg ttc tcg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly Cys Leu Val Phe Ser 280 285 290			920
att tgg tac ccg ttg ctt gtt tct tgt ttg cct aat tgg ggt gaa aga Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro Asn Trp Gly Glu Arg 295 300 305			968
att atg ttt gtt att gca agt tta tca gtg act gga atg caa caa gtt Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr Gly Met Gln Gln Val 310 315 320 325			1016
cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val Tyr Val Gly Lys Pro 330 335 340			1064
aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile 345 350 355			1112
tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln 360 365 370			1160
att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys 375 380 385			1208
atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr 390 395 400 405			1256
aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu 410 415 420			1304
agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys 425 430 435			1352
aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt Asn Leu Val Trp Glu Ala Leu His Thr His Gly 440 445			1398
agttcatgta ataatttgag attatgtatc tcctatgttt gtgtcttgtc ttggttctac			1458
ttgttgaggat cattgcaact tgtcttttat ggtttattag atgtttttta atatatttta			1518
gaggttttgc tttcatctcc attattgatg aataaggagt tgcattattgt caattgttgt			1578

gctcaatatc tgatattttg gaatgtactt tgtaccactg tgttttcagt tgaagctcat 1638
 gtgtacttct atagactttg tttaaagtgt tatgtcatgt tattt 1683

<210> 18
 <211> 448
 <212> PRT
 <213> Borago officinalis

<400> 18

Met Ala Ala Gln Ile Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn
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His Asp Lys Pro Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr
 20 25 30

Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu
 35 40 45

Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His
 50 55 60

Pro Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr
 65 70 75 80

Leu Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu
 85 90 95

Val Phe Glu Phe Ser Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile
 100 105 110

Met Phe Ala Thr Leu Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val
 115 120 125

Tyr Gly Val Leu Phe Cys Glu Gly Val Leu Val His Leu Phe Ser Gly
 130 135 140

Cys Leu Met Gly Phe Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp
 145 150 155 160

Ala Gly His Tyr Met Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met
 165 170 175

Gly Ile Phe Ala Ala Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp
 180 185 190

Lys Trp Asn His Asn Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr
 195 200 205

Asp Pro Asp Leu Gln Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe
 210 215 220

32

Phe Gly Ser Leu Thr Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp
 225 230 235 240

Ser Leu Ser Arg Phe Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro
 245 250 255

Ile Met Cys Ala Ala Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met
 260 265 270

Leu Leu Thr Lys Arg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly
 275 280 285

Cys Leu Val Phe Ser Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro
 290 295 300

Asn Trp Gly Glu Arg Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr
 305 310 315 320

Gly Met Gln Gln Val Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val
 325 330 335

Tyr Val Gly Lys Pro Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp
 340 345 350

Gly Thr Leu Asp Ile Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly
 355 360 365

Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg
 370 375 380

Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys
 385 390 395 400

His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met
 405 410 415

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr
 420 425 430

Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly
 435 440 445

<210> 19
 <211> 1563
 <212> DNA
 <213> Ceratodon purpureus

<220>
 <221> CDS
 <222> (1)..(1563)
 <223> Delta-6-Desaturase

<400> 19

33

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Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn	
1 5 10 15	
att gac gtt gag cac ttg gca acg atg ccc ctc gtc agt gac ttc cta	96
Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu	
20 25 30	
aat gtc ctg gga acg act ttg ggc cag tgg agt ctt tcc act aca ttc	144
Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe	
35 40 45	
gct ttc aag agg ctc acg act aag aaa cac agt tcg gac atc tcg gtg	192
Ala Phe Lys Arg Leu Thr Lys Lys His Ser Ser Asp Ile Ser Val	
50 55 60	
gag gca caa aaa gaa tcg gtt gcg cgg ggg cca gtt gag aat att tct	240
Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser	
65 70 75 80	
caa tcg gtt gcg cag ccc atc agg cgg agg tgg gtg cag gat aaa aag	288
Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys	
85 90 95	
ccg gtt act tac agc ctg aag gat gta gct tcg cac gat atg ccc cag	336
Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln	
100 105 110	
gac tgc tgg att ata atc aaa gag aag gtg tat gat gtg agc acc ttc	384
Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe	
115 120 125	
gct gag cag cac cct gga ggc acg gtt atc aac acc tac ttc gga cga	432
Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg	
130 135 140	
gac gcc aca gat gtt ttc tct act ttc cac gca tcc acc tca tgg aag	480
Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys	
145 150 155 160	
att ctt cag aat ttc tac atc ggg aac ctt gtt agg gag gag ccg act	528
Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr	
165 170 175	
ttg gag ctg ctg aag gag tac aga gag ttg aga gcc ctt ttc ttg aga	576
Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg	
180 185 190	
gaa cag ctt ttc aag agt tcc aaa tcc tac tac ctt ttc aag act ctc	624
Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu	
195 200 205	
ata aat gtt tcc att gtt gcc aca agc att gcg ata atc agt ctg tac	672
Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr	
210 215 220	
aag tct tac cgg gcg gtt ctg tta tca gcc agt ttg atg ggc ttg ttt	720
Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe	
225 230 235 240	
att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta	768
Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val	
245 250 255	
ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac	816
Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn	
260 265 270	

34

gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu 275 280 285	864
cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp 290 295 300	912
gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu 305 310 315 320	960
gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His 325 330 335	1008
cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe 340 345 350	1056
tgg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys 355 360 365	1104
ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser 370 375 380	1152
gtt gcg ttt tat ctg ctc ccc gga tgg aaa cca gtt gta tgg atg gtg Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val 385 390 395 400	1200
gtc agc gag ctc atg tct ggt ttc ctg ctg gga tac gta ttt gta ctc Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu 405 410 415	1248
agt cac aat gga atg gag gtg tac aat acg tca aag gac ttc gtg aat Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn 420 425 430	1296
gcc cag att gca tcg act cgc gac atc aaa gca ggg gtg ttt aat gat Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp 435 440 445	1344
tgg ttc acc gga ggt ctc aac aga cag att gag cat cat cta ttt cca Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro 450 455 460	1392
acg atg ccc agg cac aac ctt aat aaa att tct cct cac gtg gag act Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr 465 470 475 480	1440
ttg tgc aag aag cat gga ctg gtc tac gaa gac gtg agc atg gct tcg Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser 485 490 495	1488
ggc act tac ccg gtt ttg aaa aca ctt aag gac gtt gcc gat gct gct Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala 500 505 510	1536
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<210> 20
 <211> 520
 <212> PRT

<213> Ceratodon purpureus

<400> 20

Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn
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Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu
20 25 30

Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe
35 40 45

Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val
50 55 60

Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser
65 70 75 80

Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys
85 90 95

Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln
100 105 110

Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe
115 120 125

Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg
130 135 140

Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys
145 150 155 160

Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr
165 170 175

Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg
180 185 190

Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu
195 200 205

Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr
210 215 220

Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe
225 230 235 240

Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val
245 250 255

36

Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn
 260 265 270

Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu
 275 280 285

His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp
 290 295 300

Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu
 305 310 315 320

Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His
 325 330 335

Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe
 340 345 350

Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys
 355 360 365

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser
 370 375 380

Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val
 385 390 395 400

Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu
 405 410 415

Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn
 420 425 430

Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp
 435 440 445

Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro
 450 455 460

Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr
 465 470 475 480

Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser
 485 490 495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala
 500 505 510

Ser His Gln Gln Leu Ala Ala Ser
 515 520

<210> 21
 <211> 1434
 <212> DNA
 <213> *Phaeodactylum tricornutum*

<220>
 <221> CDS
 <222> (1)..(1434)
 <223> Delta-6-Desaturase

<400> 21
 atg ggc aaa gga ggg gac gct cgg gcc tcg aag ggc tca acg gcg gct 48
 Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala
 1 5 10 15
 cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac 96
 Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp
 20 25 30
 gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac 144
 Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His
 35 40 45
 gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg 192
 Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met
 50 55 60
 acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg 240
 Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met
 65 70 75 80
 aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag 288
 Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu
 85 90 95
 ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa 336
 Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys
 100 105 110
 ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac 384
 Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr
 115 120 125
 aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc 432
 Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
 130 135 140
 ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg 480
 Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu
 145 150 155 160
 gga aca ttc ttt cag cag tcg gga tgg ttg gca cac gac ttt ctg cac 528
 Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
 165 170 175
 cac cag gtc ttc acc aag cgc aag cac ggg gat ctc gga gga ctc ttt 576
 His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe
 180 185 190
 tgg ggg aac ctc atg cag ggt tac tcc gta cag tgg tgg aaa aac aag 624
 Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
 195 200 205
 cac aac gga cac cac gcc gtc ccc aac ctc cac tgc tcc tcc gca gtc 672
 His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
 210 215 220

gcg caa gat ggg gac ccg gac atc gat acc atg ccc ctt ctc gcc tgg Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp 225 230 235 240	720
tcc gtc cag caa gcc cag tct tac cgg gaa ctc caa gcc gac gga aag Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys 245 250 255	768
gat tcg ggt ttg gtc aag ttc atg atc cgt aac caa tcc tac ttt tac Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr 260 265 270	816
ttt ccc atc ttg ttg ctc gcc cgc ctg tcg tgg ttg aac gag tcc ttc Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe 275 280 285	864
aag tgc gcc ttt ggg ctt gga gct gcg tcg gag aac gct gct ctc gaa Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu 290 295 300	912
ctc aag gcc aag ggt ctt cag tac ccc ctt ttg gaa aag gct ggc atc Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile 305 310 315 320	960
ctg ctg cac tac gct tgg atg ctt aca gtt tcg tcc ggc ttt gga cgc Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg 325 330 335	1008
ttc tcg ttc gcg tac acc gca ttt tac ttt cta acc gcg acc gcg tcc Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser 340 345 350	1056
tgt gga ttc ttg ctc gcc att gtc ttt ggc ctc ggc cac aac ggc atg Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met 355 360 365	1104
gcc acc tac aat gcc gac gcc cgt ccg gac ttc tgg aag ctc caa gtc Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val 370 375 380	1152
acc acg act cgc aac gtc acg ggc gga cac ggt ttc ccc caa gcc ttt Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe 385 390 395 400	1200
gtc gac tgg ttc tgt ggt ggc ctc cag tac caa gtc gac cac cac tta Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu 405 410 415	1248
ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca cac gca ctg gtc Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val 420 425 430	1296
gaa tcg ttc tgc aag gag tgg ggt gtc cag tac cac gaa gcc gac ctt Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu 435 440 445	1344
gtg gac ggg acc atg gaa gtc ttg cac cat ttg ggc agc gtg gcc ggc Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly 450 455 460	1392
gaa ttc gtc gtg gat ttt gta cgc gat gga ccc gcc atg taa Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met 465 470 475	1434

<210> 22
<211> 477
<212> PRT

<213> Phaeodactylum tricornutum

<400> 22

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala
1 5 10 15

Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp
20 25 30

Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His
35 40 45

Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met
50 55 60

Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met
65 70 75 80

Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu
85 90 95

Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys
100 105 110

Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr
115 120 125

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
130 135 140

Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu
145 150 155 160

Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe
180 185 190

Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
195 200 205

His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
210 215 220

Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp
225 230 235 240

Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys
245 250 255

40

Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr
260 265 270

Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe
275 280 285

Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu
290 295 300

Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile
305 310 315 320

Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg
325 330 335

Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser
340 345 350

Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met
355 360 365

Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val
370 375 380

Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe
385 390 395 400

Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu
405 410 415

Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val
420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu
435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly
450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
465 470 475

<210> 23
<211> 1578
<212> DNA
<213> *Physcomitrella patens*

<220>
<221> CDS
<222> (1)..(1578)
<223> Delta-6-Desaturase

<400> 23

atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac	48
Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn	
1 5 10 15	
atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc	96
Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe	
20 25 30	
agt tat gtg tct tca act gtt ggt tcg tgg agc gta cac agt ata caa	144
Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln	
35 40 45	
cct ttg aag cgc ctg acg agt aag aag cgt gtt tcg gaa agc gct gcc	192
Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala	
50 55 60	
gtg caa tgt ata tca gct gaa gtt cag aga aat tcg agt acc cag gga	240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly	
65 70 75 80	
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg	288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg	
85 90 95	
tca tct cag tgg aag aag tcg aca cac ccc cta tca gaa gta gca gta	336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val	
100 105 110	
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat	384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr	
115 120 125	
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt	432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser	
130 135 140	
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca	480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala	
145 150 155 160	
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag	528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu	
165 170 175	
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga	576
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg	
180 185 190	
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat	624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr	
195 200 205	
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca	672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala	
210 215 220	
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt	720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys	
225 230 235 240	
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt	768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe	
245 250 255	
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg	816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly	
260 265 270	

tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys 275 280 285	864
gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr 290 295 300	912
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp 305 310 315 320	960
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile 325 330 335	1008
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg 340 345 350	1056
ggc agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu 355 360 365	1104
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr 370 375 380	1152
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro 385 390 395 400	1200
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly 405 410 415	1248
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser 420 425 430	1296
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly 435 440 445	1344
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu 450 455 460	1392
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala 465 470 475 480	1440
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp 485 490 495	1488
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu 500 505 510	1536
gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser 515 520 525	1578

<210> 24
 <211> 525
 <212> PRT

<213> Physcomitrella patens

<400> 24

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
1 5 10 15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
20 25 30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
35 40 45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
50 55 60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
65 70 75 80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
85 90 95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
100 105 110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
115 120 125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
130 135 140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
145 150 155 160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
165 170 175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
180 185 190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
195 200 205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
210 215 220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
225 230 235 240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
245 250 255

Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
 260 265 270

Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
 275 280 285

Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
 290 295 300

Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
 305 310 315 320

Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
 340 345 350

Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
 355 360 365

Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
 370 375 380

Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
 385 390 395 400

Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
 405 410 415

Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
 420 425 430

Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly
 435 440 445

Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu
 450 455 460

His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala
 465 470 475 480

Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp
 485 490 495

Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu
 500 505 510

Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser
 515 520 525

<210> 25
 <211> 1332
 <212> DNA
 <213> *Caenorhabditis elegans*

<220>
 <221> CDS
 <222> (1)..(1332)
 <223> Delta-6-Desaturase

<400> 25
 atg gtc gtc gac aag aat gcc tcc ggg ctt cga atg aag gtc gat ggc 48
 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
 1 5 10 15

aaa tgg ctc tac ctt agc gag gaa ttg gtg aag aaa cat cca gga gga 96
 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
 20 25 30

gct gtt att gaa caa tat aga aat tcg gat gct act cat att ttc cac 144
 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
 35 40 45

gct ttc cac gaa gga tct tct cag gct tat aag caa ctt gac ctt ctg 192
 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
 50 55 60

aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa ttg gaa aag 240
 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
 65 70 75 80

aga ctt gac aaa gtt gat atc aat gta tca gca tat gat gtc agt gtt 288
 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
 85 90 95

gca caa gaa aag aaa atg gtt gaa tca ttc gaa aaa cta cga cag aag 336
 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
 100 105 110

ctt cat gat gat gga tta atg aaa gca aat gaa aca tat ttc ctg ttt 384
 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
 115 120 125

aaa gcg att tca aca ctt tca att atg gca ttt gca ttt tat ctt cag 432
 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
 130 135 140

tat ctt gga tgg tat att act tct gca tgt tta tta gca ctt gca tgg 480
 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
 145 150 155 160

caa caa ttc gga tgg tta aca cat gag ttc tgc cat caa cag cca aca 528
 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
 165 170 175

aag aac aga cct ttg aat gat act att tct ttg ttc ttt ggt aat ttc 576
 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
 180 185 190

tta caa gga ttt tca aga gat tgg tgg aag gac aag cat aac act cat 624
 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
 195 200 205

cac gct gcc aca aat gta att gat cat gac ggt gat atc gac ttg gca 672
 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
 210 215 220

46

cca ctt ttc gca ttt att cca gga gat ttg tgc aag tat aag gcc agc	720
Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser	
225 230 235 240	
ttt gaa aaa gca att ctc aag att gta cca tat caa cat ctc tat ttc	768
Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe	
245 250 255	
acc gca atg ctt cca atg ctc cgt ttc tca tgg act ggt cag tca gtt	816
Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val	
260 265 270	
caa tgg gta ttc aaa gag aat caa atg gag tac aag gtc tat caa aga	864
Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg	
275 280 285	
aat gca ttc tgg gag caa gca aca att gtt gga cat tgg gct tgg gta	912
Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val	
290 295 300	
ttc tat caa ttg ttc tta tta cca aca tgg cca ctt cgg gtt gct tat	960
Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr	
305 310 315 320	
ttc att att tca caa atg gga gga ggc ctt ttg att gct cac gta gtc	1008
Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val	
325 330 335	
act ttc aac cat aac tct gtt gat aag tat cca gcc aat tct cga att	1056
Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile	
340 345 350	
tta aac aac ttc gcc gct ctt caa att ttg acc aca cgc aac atg act	1104
Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr	
355 360 365	
cca tct cca ttc att gat tgg ctt tgg ggt gga ctc aat tat cag atc	1152
Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile	
370 375 380	
gag cac cac ttg ttc cca aca atg cca cgt tgc aat ctg aat gct tgc	1200
Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys	
385 390 395 400	
gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt cct tac ctc	1248
Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu	
405 410 415	
gtc gat gac tac ttt gac gga tat gca atg aat ttg caa caa ttg aaa	1296
Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys	
420 425 430	
aat atg gct gag cac att caa gct aaa gct gcc taa	1332
Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala	
435 440	

<210> 26

<211> 443

<212> PRT

<213> Caenorhabditis elegans

<400> 26

Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
1 5 10 15

47

Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
 20 25 30

Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
 35 40 45

Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
 50 55 60

Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
 65 70 75 80

Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
 85 90 95

Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
 100 105 110

Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
 115 120 125

Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
 130 135 140

Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
 145 150 155 160

Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
 165 170 175

Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
 180 185 190

Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
 195 200 205

His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
 210 215 220

Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
 225 230 235 240

Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
 245 250 255

Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
 260 265 270

Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
 275 280 285

48

Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
 290 295 300

Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
 305 310 315 320

Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
 325 330 335

Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
 340 345 350

Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
 355 360 365

Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
 370 375 380

Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
 385 390 395 400

Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
 405 410 415

Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys
 420 425 430

Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala
 435 440

<210> 27
 <211> 873
 <212> DNA
 <213> *Physcomitrella patens*

<220>
 <221> CDS
 <222> (1)..(873)
 <223> Delta-6-Elongase

<400> 27
 atg gag gtc gtg gag aga ttc tac ggt gag ttg gat ggg aag gtc tcg 48
 Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
 1 5 10 15
 cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 96
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20 25 30
 acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 144
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35 40 45
 gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 192
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50 55 60

49

tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg	240
Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu	
65 70 75 80	
ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt	288
Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser	
85 90 95	
ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac	336
Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr	
100 105 110	
tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att	384
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile	
115 120 125	
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc	432
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr	
130 135 140	
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac	480
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His	
145 150 155 160	
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat	528
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His	
165 170 175	
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga	576
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly	
180 185 190	
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga	624
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg	
195 200 205	
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg	672
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu	
210 215 220	
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac	720
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr	
225 230 235 240	
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att	768
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile	
245 250 255	
ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac	816
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr	
260 265 270	
gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa	864
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys	
275 280 285	
act gag tga	873
Thr Glu	
290	

<210> 28

<211> 290

<212> PRT

<213> Physcomitrella patens

<400> 28

50

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
 1 5 10 15
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
 20 25 30
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
 35 40 45
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
 50 55 60
 Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
 65 70 75 80
 Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
 85 90 95
 Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
 100 105 110
 Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
 115 120 125
 Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
 130 135 140
 Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
 145 150 155 160
 Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
 165 170 175
 His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
 180 185 190
 Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
 195 200 205
 Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu
 210 215 220
 Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr
 225 230 235 240
 Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
 245 250 255
 Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
 260 265 270

51

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
 275 280 285

Thr Glu
 290

<210> 29
 <211> 1049
 <212> DNA
 <213> Thraustochytrium

<220>
 <221> CDS
 <222> (43)..(858)
 <223> Delta-6-Elongase

<400> 29
 gaattcggca cgagagcgcg cggagcggag acctcggccg cg atg atg gag ccg 54
 Met Met Glu Pro
 1

ctc gac agg tac agg gcg ctg gcg gag ctc gcc gcg agg tac gcc agc 102
 Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala Arg Tyr Ala Ser
 5 10 15 20

tgc gcg gcc ttc aag tgg caa gtc acg tac gac gcc aag gac agc ttc 150
 Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe
 25 30 35

gtc ggg ccc ctg gga atc cgg gag ccg ctc ggg ctc ctg gtg ggc tcc 198
 Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser
 40 45 50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac 246
 Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn
 55 60 65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc 294
 Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His Asn Leu Gly Leu
 70 75 80

tgc ctc ttc tgc ggc gcc gtg tgg atc tac acg agc tac ctc atg atc 342
 Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser Tyr Leu Met Ile
 85 90 95 100

cag gat ggg cac ttt cgc agc ctc gag gcg gca acg tgc gag ccg ctc 390
 Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr Cys Glu Pro Leu
 105 110 115

aag cat ccg cac ttc cag ctc atc agc ttg ctc ttt gcg ctg tcc aag 438
 Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe Ala Leu Ser Lys
 120 125 130

atc tgg gag tgg ttc gac acg gtg ctc ctc atc gtc aag ggc aac aag 486
 Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val Lys Gly Asn Lys
 135 140 145

ctc cgc ttc ctg cac gtc ttg cac cac gcc acg acc ttt tgg ctc tac 534
 Leu Arg Phe Leu His Val Leu His His Ala Thr Thr Phe Trp Leu Tyr
 150 155 160

gcc atc gac cac atc ttt ctc tgc tcc atc aag tac ggc gtc gcg gtc 582
 Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr Gly Val Ala Val
 165 170 175 180

52

aat gct ttc atc cac acc gtc atg tac gcg cac tac ttc cgc cca ttc 630
 Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr Phe Arg Pro Phe
 185 190 195
 ccg aag ggc ttg cgc ccg ctt att acg cag ttg cag atc gtc cag ttc 678
 Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln Ile Val Gln Phe
 200 205 210
 att ttc agc atc ggc atc cat acc gcc att tac tgg cac tac gac tgc 726
 Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp His Tyr Asp Cys
 215 220 225
 gag ccg ctc gtg cat acc cac ttt tgg gaa tac gtc acg ccc tac ctt 774
 Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu
 230 235 240
 ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag 822
 Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln
 245 250 255 260
 tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca 868
 Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala
 265 270
 gtagaccagc agcgccgagg acgcgtgccg cgttatcgcg aagcacgaaa taaagaagat 928
 catttgattc aacgaggcta cttgcggcca cgagaaaaaaaa aaaaaaaaaa aaaaaaaaaa 988
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1048
 c 1049

<210> 30
 <211> 271
 <212> PRT
 <213> Thraustochytrium

<400> 30

Met Met Glu Pro Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala
 1 5 10 15
 Arg Tyr Ala Ser Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala
 20 25 30
 Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu
 35 40 45
 Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr
 50 55 60
 Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His
 65 70 75 80
 Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser
 85 90 95
 Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr
 100 105 110

53

Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe
 115 120 125

Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val
 130 135 140

Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr
 145 150 155 160

Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr
 165 170 175

Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr
 180 185 190

Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln
 195 200 205

Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp
 210 215 220

His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val
 225 230 235 240

Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe
 245 250 255

Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala
 260 265 270

<210> 31
 <211> 837
 <212> DNA
 <213> Phytophthora infestans

<220>
 <221> CDS
 <222> (1)..(837)
 <223> Delta-6-Elongase

<400> 31
 atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg 48
 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr
 1 5 10 15

gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg 96
 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val
 20 25 30

cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc 144
 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala
 35 40 45

atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg 192
 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met
 50 55 60

54

aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac 240
 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr
 65 70 75 80

aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc 288
 Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala
 85 90 95

atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt 336
 Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe
 100 105 110

aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc 384
 Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu
 115 120 125

tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag 432
 Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys
 130 135 140

aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg 480
 Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
 145 150 155 160

ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca 528
 Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
 165 170 175

tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act 576
 Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
 180 185 190

tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac 624
 Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
 195 200 205

ctc acg cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc 672
 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
 210 215 220

tac ctg acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg 720
 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
 225 230 235 240

ctc atg tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat 768
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
 245 250 255

ttc tac att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag 816
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
 260 265 270

gaa tcg aag aag aag ttg taa 837
 Glu Ser Lys Lys Lys Leu
 275

<210> 32
 <211> 278
 <212> PRT
 <213> Phytophthora infestans

<400> 32

Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr
 1 5 10 15

55

Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val
 20 25 30

His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala
 35 40 45

Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met
 50 55 60

Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr
 65 70 75 80

Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala
 85 90 95

Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe
 100 105 110

Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu
 115 120 125

Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys
 130 135 140

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
 145 150 155 160

Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
 165 170 175

Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
 180 185 190

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
 195 200 205

Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
 210 215 220

Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
 225 230 235 240

Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
 245 250 255

Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
 260 265 270

Glu Ser Lys Lys Lys Leu
 275

<210> 33
 <211> 954
 <212> DNA
 <213> Mortierella alpina

<220>
 <221> CDS
 <222> (1)..(954)
 <223> Delta-6-Elongase

<400> 33
 atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc 48
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
 1 5 10 15
 ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc 96
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val
 20 25 30
 acc gga aag tcc atc gac tcc ttc gtc ttc cag gag ggc gtc acg cct 144
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro
 35 40 45
 ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc 192
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val
 50 55 60
 gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag 240
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys
 65 70 75 80
 ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc 288
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser
 85 90 95
 gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc 336
 Gly Ser Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala
 100 105 110
 aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag 384
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln
 115 120 125
 cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag 432
 Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu
 130 135 140
 ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc 480
 Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe
 145 150 155 160
 ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag 528
 Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln
 165 170 175
 ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg 576
 Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu
 180 185 190
 act gtc cac gtc ttc atg tac tac tac tac atg cgc tcc gct gcc ggt 624
 Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly
 195 200 205
 gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag 672
 Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln
 210 215 220

57

ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc 720
 Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe
 225 230 235 240
 gcc ttc acc tac ttc ccc tgg gct ccc aac gtc ggc aag tgc gcc ggt 768
 Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly
 245 250 255
 acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc 816
 Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu
 260 265 270
 ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag 864
 Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys
 275 280 285
 gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc 912
 Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser
 290 295 300
 ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa 954
 Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile
 305 310 315

<210> 34
 <211> 317
 <212> PRT
 <213> Mortierella alpina
 <400> 34

Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro
 1 5 10 15
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val
 20 25 30
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro
 35 40 45
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val
 50 55 60
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys
 65 70 75 80
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser
 85 90 95
 Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala
 100 105 110
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln
 115 120 125
 Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu
 130 135 140

58

Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe
 145 150 155 160

Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln
 165 170 175

Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu
 180 185 190

Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly
 195 200 205

Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln
 210 215 220

Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe
 225 230 235 240

Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly
 245 250 255

Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu
 260 265 270

Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys
 275 280 285

Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser
 290 295 300

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile
 305 310 315

<210> 35
 <211> 957
 <212> DNA
 <213> Mortierella alpina

<220>
 <221> CDS
 <222> (1)..(957)
 <223> Delta-6-Elongase

<400> 35
 atg gag tcg att gcg cca ttc ctc cca tca aag atg ccg caa gat ctg 48
 Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu
 1 5 10 15
 ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc 96
 Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val
 20 25 30
 gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc 144
 Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro
 35 40 45

acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro 50 55 60	192
ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile 65 70 75 80	240
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys 85 90 95	288
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe 100 105 110	336
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu 115 120 125	384
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr 130 135 140	432
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser 145 150 155 160	480
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn 165 170 175	528
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe 180 185 190	576
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr 195 200 205	624
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr 210 215 220	672
tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe 225 230 235 240	720
tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln 245 250 255	768
tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr 260 265 270	816
ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu 275 280 285	864
ggt ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln 290 295 300	912
gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln 305 310 315	957

<210> 36
 <211> 318
 <212> PRT
 <213> Mortierella alpina

<400> 36

Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu
 1 5 10 15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val
 20 25 30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro
 35 40 45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro
 50 55 60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile
 65 70 75 80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys
 85 90 95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe
 100 105 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu
 115 120 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr
 130 135 140

Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser
 145 150 155 160

Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn
 165 170 175

Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe
 180 185 190

Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr
 195 200 205

Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr
 210 215 220

Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe
 225 230 235 240

61

Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln
 245 250 255

Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr
 260 265 270

Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu
 275 280 285

Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln
 290 295 300

Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln
 305 310 315

<210> 37
 <211> 867
 <212> DNA
 <213> Caenorhabditis elegans

<220>
 <221> CDS
 <222> (1)..(867)
 <223> Delta-6-Elongase

<400> 37
 atg gct cag cat ccg ctc gtt caa cgg ctt ctc gat gtc aaa ttc gac 48
 Met Ala Gln His Pro Leu Val Gln Arg Leu Leu Asp Val Lys Phe Asp
 1 5 10 15
 acg aaa cga ttt gtg gct att gct act cat ggg cca aag aat ttc cct 96
 Thr Lys Arg Phe Val Ala Ile Ala Thr His Gly Pro Lys Asn Phe Pro
 20 25 30
 gac gca gaa ggt cgc aag ttc ttt gct gat cac ttt gat gtt act att 144
 Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile
 35 40 45
 cag gct tca atc ctg tac atg gtc gtt gtg ttc gga aca aaa tgg ttc 192
 Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe
 50 55 60
 atg cgt aat cgt caa cca ttc caa ttg act att cca ctc aac atc tgg 240
 Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp
 65 70 75 80
 aat ttc atc ctc gcc gca ttt tcc atc gca gga gct gtc aaa atg acc 288
 Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr
 85 90 95
 cca gag ttc ttt gga acc att gcc aac aaa gga att gtc gca tcc tac 336
 Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr
 100 105 110
 tgc aaa gtg ttt gat ttc acg aaa gga gag aat gga tac tgg gtg tgg 384
 Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp
 115 120 125
 ctc ttc atg gct tcc aaa ctt ttc gaa ctt gtt gac acc atc ttc ttg 432
 Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu
 130 135 140

62

gtt ctc cgt aaa cgt cca ctc atg ttc ctt cac tgg tat cac cat att 480
Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile
145 150 155 160

ctc acc atg atc tac gcc tgg tac tct cat cca ttg acc cca gga ttc 528
Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe
165 170 175

aac aga tac gga att tat ctt aac ttt gtc gtc cac gcc ttc atg tac 576
Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr
180 185 190

tct tac tac ttc ctt cgc tcg atg aag att cgc gtg cca gga ttc atc 624
Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile
195 200 205

gcc caa gct atc aca tct ctt caa atc gtt caa ttc atc atc tct tgc 672
Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys
210 215 220

gcc gtt ctt gct cat ctt ggt tat ctc atg cac ttc acc aat gcc aac 720
Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn
225 230 235 240

tgt gat ttc gag cca tca gta ttc aag ctc gca gtt ttc atg gac aca 768
Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr
245 250 255

aca tac ttg gct ctt ttc gtc aac ttc ttc ctc caa tca tat gtt ctc 816
Thr Tyr Leu Ala Leu Phe Val Asn Phe Phe Leu Gln Ser Tyr Val Leu
260 265 270

cgc gga gga aaa gac aag tac aag gca gtg cca aag aag aag aac aac 864
Arg Gly Gly Lys Asp Lys Tyr Lys Ala Val Pro Lys Lys Lys Asn Asn
275 280 285

taa 867

<210> 38
<211> 288
<212> PRT
<213> Caenorhabditis elegans

<400> 38

Met Ala Gln His Pro Leu Val Gln Arg Leu Leu Asp Val Lys Phe Asp
1 5 10 15

Thr Lys Arg Phe Val Ala Ile Ala Thr His Gly Pro Lys Asn Phe Pro
20 25 30

Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile
35 40 45

Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe
50 55 60

Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp
65 70 75 80

Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr
85 90 95

Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr
 100 105 110

Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp
 115 120 125

Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu
 130 135 140

Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile
 145 150 155 160

Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe
 165 170 175

Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr
 180 185 190

Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile
 195 200 205

Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys
 210 215 220

Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn
 225 230 235 240

Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr
 245 250 255

Thr Tyr Leu Ala Leu Phe Val Asn Phe Phe Leu Gln Ser Tyr Val Leu
 260 265 270

Arg Gly Gly Lys Asp Lys Tyr Lys Ala Val Pro Lys Lys Lys Asn Asn
 275 280 285

<210> 39
 <211> 1626
 <212> DNA
 <213> Euglena gracilis

<220>
 <221> CDS
 <222> (1)..(1626)
 <223> Delta-4-Desaturase

<400> 39
 atg ttg gtg ctg ttt ggc aat ttc tat gtc aag caa tac tcc caa aag
 Met Leu Val Leu Phe Gly Asn Phe Tyr Val Lys Gln Tyr Ser Gln Lys
 1 5 10 15

aac ggc aag ccg gag aac gga gcc acc cct gag aac gga gcg aag ccg
 Asn Gly Lys Pro Glu Asn Gly Ala Thr Pro Glu Asn Gly Ala Lys Pro

48

96

20	25	30	
caa cct tgc gag aac ggc acg gtg gaa aag cga gag aat gac acc gcc Gln Pro Cys Glu Asn Gly Thr Val Glu Lys Arg Glu Asn Asp Thr Ala 35 40 45			144
aac gtt cgg ccc acc cgt cca gct gga ccc ccg ccg gcc acg tac tac Asn Val Arg Pro Thr Arg Pro Ala Gly Pro Pro Pro Ala Thr Tyr Tyr 50 55 60			192
gac tcc ctg gca gtg tcg ggg cag ggc aag gag cgg ctg ttc acc acc Asp Ser Leu Ala Val Ser Gly Gln Gly Lys Glu Arg Leu Phe Thr Thr 65 70 75 80			240
gat gag gtg agg cgg cac atc ctc ccc acc gat ggc tgg ctg acg tgc Asp Glu Val Arg Arg His Ile Leu Pro Thr Asp Gly Trp Leu Thr Cys 85 90 95			288
cac gaa gga gtc tac gat gtc act gat ttc ctt gcc aag cac cct ggt His Glu Gly Val Tyr Asp Val Thr Asp Phe Leu Ala Lys His Pro Gly 100 105 110			336
ggc ggt gtc atc acg ctg ggc ctt gga agg gac tgc aca atc ctc atc Gly Gly Val Ile Thr Leu Gly Leu Gly Arg Asp Cys Thr Ile Leu Ile 115 120 125			384
gag tca tac cac cct gct ggg cgc ccg gac aag gtg atg gag aag tac Glu Ser Tyr His Pro Ala Gly Arg Pro Asp Lys Val Met Glu Lys Tyr 130 135 140			432
cgc att ggt acg ctg cag gac ccc aag acg ttc tat gct tgg gga gag Arg Ile Gly Thr Leu Gln Asp Pro Lys Thr Phe Tyr Ala Trp Gly Glu 145 150 155 160			480
tcc gat ttc tac cct gag ttg aag cgc cgg gcc ctt gca agg ctg aag Ser Asp Phe Tyr Pro Glu Leu Lys Arg Arg Ala Leu Ala Arg Leu Lys 165 170 175			528
gag gct ggt cag gcg cgg cgc ggc ggc ctt ggg gtg aag gcc ctc ctg Glu Ala Gly Gln Ala Arg Arg Gly Gly Leu Gly Val Lys Ala Leu Leu 180 185 190			576
gtg ctc acc ctc ttc ttc gtg tcg tgg tac atg tgg gtg gcc cac aag Val Leu Thr Leu Phe Phe Val Ser Trp Tyr Met Trp Val Ala His Lys 195 200 205			624
tcc ttc ctc tgg gcc gcc gtc tgg ggc ttc gcc ggc tcc cac gtc ggg Ser Phe Leu Trp Ala Ala Val Trp Gly Phe Ala Gly Ser His Val Gly 210 215 220			672
ctg agc atc cag cac gat ggc aac cac ggc gcg ttc agc cgc aac aca Leu Ser Ile Gln His Asp Gly Asn His Gly Ala Phe Ser Arg Asn Thr 225 230 235 240			720
ctg gtg aac cgc ctg gcg ggg tgg ggc atg gac ttg atc ggc gcg tcg Leu Val Asn Arg Leu Ala Gly Trp Gly Met Asp Leu Ile Gly Ala Ser 245 250 255			768
tcc acg gtg tgg gag tac cag cac gtc atc ggc cac cac cag tac acc Ser Thr Val Trp Glu Tyr Gln His Val Ile Gly His His Gln Tyr Thr 260 265 270			816
aac ctc gtg tcg gac acg cta ttc agt ctg cct gag aac gat ccg gac Asn Leu Val Ser Asp Thr Leu Phe Ser Leu Pro Glu Asn Asp Pro Asp 275 280 285			864
gtc ttc tcc agc tac ccg ctg atg cgc atg cac ccg gat acg gcg tgg Val Phe Ser Ser Tyr Pro Leu Met Arg Met His Pro Asp Thr Ala Trp			912

65

290	295	300	
cag ccg cac cac cgc ttc	cag cac ctg ttc	gcg ttc cca ctg ttc gcc	960
Gln Pro His His Arg Phe	Gln His Leu Phe	Ala Phe Pro Leu Phe Ala	
305	310	315 320	
ctg atg aca atc agc aag	gtg ctg acc agc gat ttc	gct gtc tgc ctc	1008
Leu Met Thr Ile Ser Lys	Val Leu Thr Ser Asp Phe	Ala Val Cys Leu	
	325	330 335	
agc atg aag aag ggg tcc	atc gac tgc tcc tcc	agg ctc gtc cca ctg	1056
Ser Met Lys Lys Gly Ser	Ile Asp Cys Ser Ser	Arg Leu Val Pro Leu	
	340	345 350	
gag ggg cag ctg ctg ttc	tgg ggg gcc aag ctg	gcg aac ttc ctg ttg	1104
Glu Gly Gln Leu Leu Phe	Trp Gly Ala Lys Leu	Ala Asn Phe Leu Leu	
	355	360 365	
cag att gtg ttg cca tgc	tac ctc cac ggg aca	gct atg ggc ctg gcc	1152
Gln Ile Val Leu Pro Cys	Tyr Leu His Gly Thr	Ala Met Gly Leu Ala	
	370	375 380	
ctc ttc tct gtt gct cac	ctt gtg tgc ggg gag	tac ctc gcg atc tgc	1200
Leu Phe Ser Val Ala His	Leu Val Ser Gly Glu	Tyr Leu Ala Ile Cys	
	385	390 395 400	
ttc atc atc aac cac atc	agc gag tct tgt gag	ttt atg aat aca agc	1248
Phe Ile Ile Asn His Ile	Ser Glu Ser Cys Glu	Phe Met Asn Thr Ser	
	405	410 415	
ttt caa acc gcc gcc cgg	agg aca gag atg ctt	cag gca gca cat cag	1296
Phe Gln Thr Ala Ala Arg	Arg Thr Glu Met Leu	Gln Ala Ala His Gln	
	420	425 430	
gca gcg gag gcc aag aag	gtg aag ccc acc cct	cca ccg aac gat tgg	1344
Ala Ala Glu Ala Lys Lys	Val Lys Pro Thr Pro	Pro Pro Asn Asp Trp	
	435	440 445	
gct gtg aca cag gtc caa	tgc tgc gtg aat tgg	aga tca ggt ggc gtg	1392
Ala Val Thr Gln Val Gln	Cys Cys Val Asn Trp	Arg Ser Gly Gly Val	
	450	455 460	
ttg gcc aat cac ctc tct	gga ggc ttg aac cac	cag atc gag cat cat	1440
Leu Ala Asn His Leu Ser	Gly Gly Leu Asn His	Gln Ile Glu His His	
	465	470 475 480	
ctg ttc ccc agc atc tgc	cat gcc aac tac ccc	acc atc gcc cct gtt	1488
Leu Phe Pro Ser Ile Ser	His Ala Asn Tyr Pro	Thr Ile Ala Pro Val	
	485	490 495	
gtg aag gag gtg tgc gag	gag tac ggg ttg ccg	tac aag aat tac gtc	1536
Val Lys Glu Val Cys Glu	Glu Tyr Gly Leu Pro	Tyr Lys Asn Tyr Val	
	500	505 510	
acg ttc tgg gat gca gtc	tgt ggc atg gtt cag	cac ctc cgg ttg atg	1584
Thr Phe Trp Asp Ala Val	Cys Gly Met Val Gln	His Leu Arg Leu Met	
	515	520 525	
ggt gct cca ccg gtg cca	acg aac ggg gac aaa	aag tca taa	1626
Gly Ala Pro Pro Val Pro	Thr Asn Gly Asp Lys	Lys Ser	
	530	535 540	

<210> 40

<211> 541

<212> PRT

<213> Euglena gracilis

<400> 40

Met Leu Val Leu Phe Gly Asn Phe Tyr Val Lys Gln Tyr Ser Gln Lys
1 5 10 15

Asn Gly Lys Pro Glu Asn Gly Ala Thr Pro Glu Asn Gly Ala Lys Pro
20 25 30

Gln Pro Cys Glu Asn Gly Thr Val Glu Lys Arg Glu Asn Asp Thr Ala
35 40 45

Asn Val Arg Pro Thr Arg Pro Ala Gly Pro Pro Pro Ala Thr Tyr Tyr
50 55 60

Asp Ser Leu Ala Val Ser Gly Gln Gly Lys Glu Arg Leu Phe Thr Thr
65 70 75 80

Asp Glu Val Arg Arg His Ile Leu Pro Thr Asp Gly Trp Leu Thr Cys
85 90 95

His Glu Gly Val Tyr Asp Val Thr Asp Phe Leu Ala Lys His Pro Gly
100 105 110

Gly Gly Val Ile Thr Leu Gly Leu Gly Arg Asp Cys Thr Ile Leu Ile
115 120 125

Glu Ser Tyr His Pro Ala Gly Arg Pro Asp Lys Val Met Glu Lys Tyr
130 135 140

Arg Ile Gly Thr Leu Gln Asp Pro Lys Thr Phe Tyr Ala Trp Gly Glu
145 150 155 160

Ser Asp Phe Tyr Pro Glu Leu Lys Arg Arg Ala Leu Ala Arg Leu Lys
165 170 175

Glu Ala Gly Gln Ala Arg Arg Gly Gly Leu Gly Val Lys Ala Leu Leu
180 185 190

Val Leu Thr Leu Phe Phe Val Ser Trp Tyr Met Trp Val Ala His Lys
195 200 205

Ser Phe Leu Trp Ala Ala Val Trp Gly Phe Ala Gly Ser His Val Gly
210 215 220

Leu Ser Ile Gln His Asp Gly Asn His Gly Ala Phe Ser Arg Asn Thr
225 230 235 240

Leu Val Asn Arg Leu Ala Gly Trp Gly Met Asp Leu Ile Gly Ala Ser
245 250 255

Ser Thr Val Trp Glu Tyr Gln His Val Ile Gly His His Gln Tyr Thr
260 265 270

Asn Leu Val Ser Asp Thr Leu Phe Ser Leu Pro Glu Asn Asp Pro Asp
275 280 285

Val Phe Ser Ser Tyr Pro Leu Met Arg Met His Pro Asp Thr Ala Trp
290 295 300

Gln Pro His His Arg Phe Gln His Leu Phe Ala Phe Pro Leu Phe Ala
305 310 315 320

Leu Met Thr Ile Ser Lys Val Leu Thr Ser Asp Phe Ala Val Cys Leu
325 330 335

Ser Met Lys Lys Gly Ser Ile Asp Cys Ser Ser Arg Leu Val Pro Leu
340 345 350

Glu Gly Gln Leu Leu Phe Trp Gly Ala Lys Leu Ala Asn Phe Leu Leu
355 360 365

Gln Ile Val Leu Pro Cys Tyr Leu His Gly Thr Ala Met Gly Leu Ala
370 375 380

Leu Phe Ser Val Ala His Leu Val Ser Gly Glu Tyr Leu Ala Ile Cys
385 390 395 400

Phe Ile Ile Asn His Ile Ser Glu Ser Cys Glu Phe Met Asn Thr Ser
405 410 415

Phe Gln Thr Ala Ala Arg Arg Thr Glu Met Leu Gln Ala Ala His Gln
420 425 430

Ala Ala Glu Ala Lys Lys Val Lys Pro Thr Pro Pro Asn Asp Trp
435 440 445

Ala Val Thr Gln Val Gln Cys Cys Val Asn Trp Arg Ser Gly Gly Val
450 455 460

Leu Ala Asn His Leu Ser Gly Gly Leu Asn His Gln Ile Glu His His
465 470 475 480

Leu Phe Pro Ser Ile Ser His Ala Asn Tyr Pro Thr Ile Ala Pro Val
485 490 495

Val Lys Glu Val Cys Glu Glu Tyr Gly Leu Pro Tyr Lys Asn Tyr Val
500 505 510

Thr Phe Trp Asp Ala Val Cys Gly Met Val Gln His Leu Arg Leu Met
515 520 525

Gly Ala Pro Pro Val Pro Thr Asn Gly Asp Lys Lys Ser
530 535 540

<210> 41
 <211> 1548
 <212> DNA
 <213> Thraustochytrium

<220>
 <221> CDS
 <222> (1)..(1548)
 <223> Delta-4-Desaturase

<400> 41
 atg acg gtc ggg ttt gac gaa acg gtg act atg gac acg gtc cgc aac 48
 Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
 1 5 10 15
 cac aac atg ccg gac gac gcc tgg tgc gcg atc cac ggc acc gtg tac 96
 His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
 20 25 30
 gac atc acc aag ttc agc aag gtg cac ccc ggc ggg gac atc atc atg 144
 Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
 35 40 45
 ctg gcc gct ggc aag gag gcc acc atc ctg ttc gag acc tac cac atc 192
 Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
 50 55 60
 aag ggc gtc ccg gac gcg gtg ctg cgc aag tac aag gtc ggc aag ctc 240
 Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
 65 70 75 80
 ccc cag ggc aag aag ggc gaa acg agc cac atg ccc acc ggc ctc gac 288
 Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp
 85 90 95
 tcg gcc tcc tac tac tcg tgg gac agc gag ttt tac agg gtg ctc cgc 336
 Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
 100 105 110
 gag cgc gtc gcc aag aag ctg gcc gag ccc ggc ctc atg cag cgc gcg 384
 Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
 115 120 125
 cgc atg gag ctc tgg gcc aag gcg atc ttc ctc ctg gca ggt ttc tgg 432
 Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
 130 135 140
 ggc tcc ctt tac gcc atg tgc gtg cta gac ccg cac ggc ggt gcc atg 480
 Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
 145 150 155 160
 gta gcc gcc gtt acg ctc ggc gtg ttc gct gcc ttt gtc gga act tgc 528
 Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys
 165 170 175
 atc cag cac gac ggc agc cac ggc gcc ttc tcc aag tcg cga ttc atg 576
 Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met
 180 185 190
 aac aag gcg gcg ggc tgg acc ctc gac atg atc ggc gcg agt gcg atg 624
 Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met
 195 200 205
 acc tgg gag atg cag cac gtt ctt ggc cac cac ccg tac acc aac ctc 672
 Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu

210	215	220	
atc gag atg gag aac ggt ttg gcc aag gtc aag ggc gcc gac gtc gac			720
Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp			
225	230	235	240
ccg aag aag gtc gac cag gag agc gac ccg gac gtc ttc agt acg tac			768
Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr			
	245	250	255
ccg atg ctt cgc ctg cac ccg tgg cac cgc cag cgg ttt tac cac aag			816
Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys			
	260	265	270
ttc cag cac ctg tac gcc ccg ttt atc ttt ggg tct atg acg att aac			864
Phe Gln His Leu Tyr Ala Pro Phe Ile Phe Gly Ser Met Thr Ile Asn			
	275	280	285
aag gtg att tcc cag gat gtc ggg gtt gtg ctg cgc aag cgc ctg ttc			912
Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe			
	290	295	300
cag atc gac gcc aac tgc cgg tat ggc agc ccc tgg tac gtg gcc cgc			960
Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Tyr Val Ala Arg			
305	310	315	320
ttc tgg atc atg aag ctc ctc acc acg ctc tac atg gtg gcg ctt ccc			1008
Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro			
	325	330	335
atg tac atg cag ggg cct gct cag ggc ttg aag ctt ttc ttc atg gcc			1056
Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala			
	340	345	350
cac ttc acc tgc gga gag gtc ctc gcc acc atg ttt att gtc aac cac			1104
His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His			
	355	360	365
atc atc gag ggc gtc agc tac gct tcc aag gac gcg gtc aag ggc gtc			1152
Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val			
	370	375	380
atg gct ccg ccg cgc act gtg cac ggt gtc acc ccg atg cag gtg acg			1200
Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr			
385	390	395	400
caa aag gcg ctc agt gcg gcc gag tcg gcc aag tcg gac gcc gac aag			1248
Gln Lys Ala Leu Ser Ala Ala Glu Ser Ala Lys Ser Asp Ala Asp Lys			
	405	410	415
acg acc atg atc ccc ctc aac gac tgg gcc gct gtg cag tgc cag acc			1296
Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr			
	420	425	430
tct gtg aac tgg gct gtc ggg tcg tgg ttt tgg aac cac ttt tcg ggc			1344
Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly			
	435	440	445
ggc ctc aac cac cag att gag cac cac tgc ttc ccc caa aac ccc cac			1392
Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His			
	450	455	460
acg gtc aac gtc tac atc tcg ggc atc gtc aag gag acc tgc gaa gaa			1440
Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu			
465	470	475	480
tac ggc gtg ccg tac cag gct gag atc agc ctc ttc tct gcc tat ttc			1488
Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe			

70

485	490	495	
aag atg ctg tcg cac ctc cgc acg ctc	ggc aac gag gac ctc acg gcc	1536	
Lys Met Leu Ser His Leu Arg Thr Leu	Gly Asn Glu Asp Leu Thr Ala		
500	505 510		
tgg tcc acg tga		1548	
Trp Ser Thr			
515			
<210> 42			
<211> 515			
<212> PRT			
<213> Thraustochytrium			
<400> 42			
Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn			
1 5 10 15			
His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr			
20 25 30			
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met			
35 40 45			
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile			
50 55 60			
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu			
65 70 75 80			
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp			
85 90 95			
Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg			
100 105 110			
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala			
115 120 125			
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp			
130 135 140			
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met			
145 150 155 160			
Val Ala Ala Val Thr Leu Gly Val Phe Ala Ala Phe Val Gly Thr Cys			
165 170 175			
Ile Gln His Asp Gly Ser His Gly Ala Phe Ser Lys Ser Arg Phe Met			
180 185 190			
Asn Lys Ala Ala Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Met			
195 200 205			

Thr Trp Glu Met Gln His Val Leu Gly His His Pro Tyr Thr Asn Leu
 210 215 220

Ile Glu Met Glu Asn Gly Leu Ala Lys Val Lys Gly Ala Asp Val Asp
 225 230 235 240

Pro Lys Lys Val Asp Gln Glu Ser Asp Pro Asp Val Phe Ser Thr Tyr
 245 250 255

Pro Met Leu Arg Leu His Pro Trp His Arg Gln Arg Phe Tyr His Lys
 260 265 270

Phe Gln His Leu Tyr Ala Pro Phe Ile Phe Gly Ser Met Thr Ile Asn
 275 280 285

Lys Val Ile Ser Gln Asp Val Gly Val Val Leu Arg Lys Arg Leu Phe
 290 295 300

Gln Ile Asp Ala Asn Cys Arg Tyr Gly Ser Pro Trp Tyr Val Ala Arg
 305 310 315 320

Phe Trp Ile Met Lys Leu Leu Thr Thr Leu Tyr Met Val Ala Leu Pro
 325 330 335

Met Tyr Met Gln Gly Pro Ala Gln Gly Leu Lys Leu Phe Phe Met Ala
 340 345 350

His Phe Thr Cys Gly Glu Val Leu Ala Thr Met Phe Ile Val Asn His
 355 360 365

Ile Ile Glu Gly Val Ser Tyr Ala Ser Lys Asp Ala Val Lys Gly Val
 370 375 380

Met Ala Pro Pro Arg Thr Val His Gly Val Thr Pro Met Gln Val Thr
 385 390 395 400

Gln Lys Ala Leu Ser Ala Ala Glu Ser Ala Lys Ser Asp Ala Asp Lys
 405 410 415

Thr Thr Met Ile Pro Leu Asn Asp Trp Ala Ala Val Gln Cys Gln Thr
 420 425 430

Ser Val Asn Trp Ala Val Gly Ser Trp Phe Trp Asn His Phe Ser Gly
 435 440 445

Gly Leu Asn His Gln Ile Glu His His Cys Phe Pro Gln Asn Pro His
 450 455 460

Thr Val Asn Val Tyr Ile Ser Gly Ile Val Lys Glu Thr Cys Glu Glu
 465 470 475 480

Tyr Gly Val Pro Tyr Gln Ala Glu Ile Ser Leu Phe Ser Ala Tyr Phe
 485 490 495

Lys Met Leu Ser His Leu Arg Thr Leu Gly Asn Glu Asp Leu Thr Ala
 500 505 510

Trp Ser Thr
 515

<210> 43
 <211> 960
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(960)
 <223> Delta-5-Elongase

<400> 43
 atg gtg ttg tac aat gtg gcg caa gtg ctg ctc aat ggg tgg acg gtg 48
 Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val
 1 5 10 15
 tat gcg att gtg gat gcg gtg atg aat aga gac cat ccg ttt att gga 96
 Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly
 20 25 30
 agt aga agt ttg gtt ggg gcg gcg ttg cat agt ggg agc tcg tat gcg 144
 Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala
 35 40 45
 gtg tgg gtt cat tat tgt gat aag tat ttg gag ttc ttt gat acg tat 192
 Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr
 50 55 60
 ttt atg gtg ttg agg ggg aaa atg gac cag atg gta ctt ggt gaa gtt 240
 Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val
 65 70 75 80
 ggt ggc agt gtg tgg tgt ggc gtt gga tat atg gat atg gag aag atg 288
 Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met
 85 90 95
 ata cta ctc agc ttt gga gtg cat cgg tct gct cag gga acg ggg aag 336
 Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys
 100 105 110
 gct ttc acc aac aac gtt acc aat cca cat ctc acg ctt cca cct cat 384
 Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His
 115 120 125
 tct aca aaa aca aaa aaa cag gtc tcc ttc ctc cac atc tac cac cac 432
 Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His
 130 135 140
 acg acc ata gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt 480
 Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly
 145 150 155 160
 gga gac att tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc 528
 Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu

165	170	175	
atg tat tcc tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg			576
Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp			
180	185	190	
aaa cga tac ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg			624
Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val			
195	200	205	
gtt tat acg ggg tgt acg ggt tat act cat tac tat cat acg aag cat			672
Val Tyr Thr Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His			
210	215	220	
gga gcg gat gag aca cag cct agt tta gga acg tat tat ttc tgt tgt			720
Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys			
225	230	235	240
gga gtg cag gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc			768
Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile			
245	250	255	
ttt tat aaa cga tcc tat tcg aag aag aac aag tca gga gga aag gat			816
Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp			
260	265	270	
agc aag aag aat gat gat ggg aat aat gag gat caa tgt cac aag gct			864
Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala			
275	280	285	
atg aag gat ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg			912
Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala			
290	295	300	
aag gat gct gga aag ttg gtg gct acg aga gta agg tgt aag gtg taa			960
Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val			
305	310	315	

<210> 44
 <211> 319
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 44

Met Val Leu Tyr Asn Val Ala Gln Val Leu Leu Asn Gly Trp Thr Val
1 5 10 15

Tyr Ala Ile Val Asp Ala Val Met Asn Arg Asp His Pro Phe Ile Gly
20 25 30

Ser Arg Ser Leu Val Gly Ala Ala Leu His Ser Gly Ser Ser Tyr Ala
35 40 45

Val Trp Val His Tyr Cys Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr
50 55 60

Phe Met Val Leu Arg Gly Lys Met Asp Gln Met Val Leu Gly Glu Val
65 70 75 80

Gly Gly Ser Val Trp Cys Gly Val Gly Tyr Met Asp Met Glu Lys Met
85 90 95

Ile Leu Leu Ser Phe Gly Val His Arg Ser Ala Gln Gly Thr Gly Lys
 100 105 110

Ala Phe Thr Asn Asn Val Thr Asn Pro His Leu Thr Leu Pro Pro His
 115 120 125

Ser Thr Lys Thr Lys Lys Gln Val Ser Phe Leu His Ile Tyr His His
 130 135 140

Thr Thr Ile Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly
 145 150 155 160

Gly Asp Ile Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu
 165 170 175

Met Tyr Ser Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp
 180 185 190

Lys Arg Tyr Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val
 195 200 205

Val Tyr Thr Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His
 210 215 220

Gly Ala Asp Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys
 225 230 235 240

Gly Val Gln Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile
 245 250 255

Phe Tyr Lys Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp
 260 265 270

Ser Lys Lys Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala
 275 280 285

Met Lys Asp Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala
 290 295 300

Lys Asp Ala Gly Lys Leu Val Ala Thr Arg Val Arg Cys Lys Val
 305 310 315

<210> 45
 <211> 819
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(819)
 <223> Delta-5-Elongase

<400> 45
 atg gac gcc tac aac gct gca atg gat aag atc ggt gcc gcc atc atc 48
 Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile
 1 5 10 15

gat tgg tct gat ccc gat gga aag ttc cgt gcc gat aga gag gac tgg 96
 Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp
 20 25 30

tgg ctc tgc gac ttc cgt agc gcc atc acc atc gcc ctc atc tac atc 144
 Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile
 35 40 45

gcc ttc gtc atc ctc ggt tcc gcc gtc atg caa tcc ctc ccc gca atg 192
 Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met
 50 55 60

gat ccc tac ccc atc aaa ttc ctc tac aac gtc tcc caa atc ttc ctt 240
 Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu
 65 70 75 80

tgt gcc tac atg act gtc gag gcg gga ttt ttg gcc tac cgc aat gga 288
 Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly
 85 90 95

tat acc gtc atg cct tgc aat cat ttc aat gtg aat gat cct ccc gtg 336
 Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val
 100 105 110

gcg aat ctt ctt tgg ttg ttt tat att tcc aag gtg tgg gac ttt tgg 384
 Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp
 115 120 125

gat acc att ttc att gtg ttg ggg aag aag tgg cgt caa tta tct ttc 432
 Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe
 130 135 140

ttg cat gta tac cat cac acc acc atc ttt cta ttc tat tgg ctg aat 480
 Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn
 145 150 155 160

gcc aat gtc ttg tac gat ggt gac atc ttc ctt acc atc ttg ctc aat 528
 Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn
 165 170 175

gga ttc atc cac acg gtg atg tac acg tat tac ttc atc tgt atg cat 576
 Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His
 180 185 190

acc aaa gat tcc aag acg ggc aag agt ctt cct ata tgg tgg aag tcg 624
 Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser
 195 200 205

agt ttg acg gcg ttt cag ttg ttg caa ttc act atc atg atg agt cag 672
 Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln
 210 215 220

gct acc tac ctt gtc ttc cac ggg tgt gat aag gtg tcg ctt cgt atc 720
 Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile
 225 230 235 240

acg att gtg tac ttt gtg tcc ctt ttg agt ttg ttc ttc ctt ttt gct 768
 Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala
 245 250 255

cag ttc ttt gtg caa tca tac atg gca ccc aaa aag aag aag agt gct 816
 Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala

260

265

270

tag

819

<210> 46
 <211> 272
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 46

Met Asp Ala Tyr Asn Ala Ala Met Asp Lys Ile Gly Ala Ala Ile Ile
 1 5 10 15

Asp Trp Ser Asp Pro Asp Gly Lys Phe Arg Ala Asp Arg Glu Asp Trp
 20 25 30

Trp Leu Cys Asp Phe Arg Ser Ala Ile Thr Ile Ala Leu Ile Tyr Ile
 35 40 45

Ala Phe Val Ile Leu Gly Ser Ala Val Met Gln Ser Leu Pro Ala Met
 50 55 60

Asp Pro Tyr Pro Ile Lys Phe Leu Tyr Asn Val Ser Gln Ile Phe Leu
 65 70 75 80

Cys Ala Tyr Met Thr Val Glu Ala Gly Phe Leu Ala Tyr Arg Asn Gly
 85 90 95

Tyr Thr Val Met Pro Cys Asn His Phe Asn Val Asn Asp Pro Pro Val
 100 105 110

Ala Asn Leu Leu Trp Leu Phe Tyr Ile Ser Lys Val Trp Asp Phe Trp
 115 120 125

Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu Ser Phe
 130 135 140

Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp Leu Asn
 145 150 155 160

Ala Asn Val Leu Tyr Asp Gly Asp Ile Phe Leu Thr Ile Leu Leu Asn
 165 170 175

Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys Met His
 180 185 190

Thr Lys Asp Ser Lys Thr Gly Lys Ser Leu Pro Ile Trp Trp Lys Ser
 195 200 205

Ser Leu Thr Ala Phe Gln Leu Leu Gln Phe Thr Ile Met Met Ser Gln
 210 215 220

Ala Thr Tyr Leu Val Phe His Gly Cys Asp Lys Val Ser Leu Arg Ile
 225 230 235 240

Thr Ile Val Tyr Phe Val Ser Leu Leu Ser Leu Phe Phe Leu Phe Ala
 245 250 255

Gln Phe Phe Val Gln Ser Tyr Met Ala Pro Lys Lys Lys Lys Ser Ala
 260 265 270

<210> 47
 <211> 936
 <212> DNA
 <213> Crypthecodinium cohnii

<220>
 <221> CDS
 <222> (1)..(936)
 <223> Delta-5-Elongase

<400> 47
 atg tct gcc ttc atg act ctc cca cag gct ctc tcc gat gtg acc tcg 48
 Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser
 1 5 10 15
 gcc ttg gtc acg ctg gga aag gat gtc tcc agc cct tca gct ttt caa 96
 Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln
 20 25 30
 gct gtc act ggc ttc tgc agg gag cag tgg ggg att ccg aca gta ttc 144
 Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe
 35 40 45
 tgc ctg ggc tac ttg gcc atg gtc tac gcg gcc aga aga ccc ctc ccg 192
 Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro
 50 55 60
 cag cac ggc tac atg gtt gcg gtg gac cgt tgc ttc gct gct tgg aac 240
 Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn
 65 70 75 80
 ttg gct ctc tct gtc ttc agc act tgg ggc ttc tac cac atg gct gtc 288
 Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val
 85 90 95
 ggg ctc tac aac atg aca gag acg agg ggc ttg caa ttc acc atc tgc 336
 Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys
 100 105 110
 ggt tcg act ggg gag ctc gtg cag aac ctt cag act ggc cca acc gct 384
 Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala
 115 120 125
 ctg gcg ctc tgc ctc ttc tgc ttc agc aag atc ccc gag ttg atg gac 432
 Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp
 130 135 140
 acg gtg ttt ctc atc ctg aag gcc aag aag gtc cgc ttc ttg cag tgg 480
 Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp
 145 150 155 160
 tac cac cat gcc aca gtc atg ctc ttc tgt tgg ctc gcc ctc gcg acg 528
 Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr
 165 170 175

gag tac act cct ggc ttg tgg ttt gcg gcg acg aac tac ttc gtg cac 576
 Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His
 180 185 190

tcc atc atg tac atg tac ttc ttc ctc atg acc ttc aag tcg gcc gcg 624
 Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala
 195 200 205

aag gtg gtg aag ccc atc gcc cct ctc atc aca gtt atc cag att gct 672
 Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala
 210 215 220

cag atg gtc tgg ggc ctc atc gtc aac ggc atc gcc atc acc acc ttc 720
 Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe
 225 230 235 240

ttc acg act ggt gcc tgc cag atc cag tct gtg act gtg tat tcg gcc 768
 Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala
 245 250 255

atc atc atg tac gct tcg tac ttc tac ctg ttc ttc cag ctc ttc ttc 816
 Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe
 260 265 270

gag gcc cat ggt gcc gct ggc aag aac aag aag aag ttg acc cgc gag 864
 Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu
 275 280 285

ctc tct cga aaa atc tcg gag gct ctc ctg aac acc ggt gac gag gtt 912
 Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val
 290 295 300

tcc aag cac ctg aag gtg aat tga 936
 Ser Lys His Leu Lys Val Asn
 305 310

<210> 48
 <211> 311
 <212> PRT
 <213> Crypthecodinium cohnii

<400> 48

Met Ser Ala Phe Met Thr Leu Pro Gln Ala Leu Ser Asp Val Thr Ser
1 5 10 15

Ala Leu Val Thr Leu Gly Lys Asp Val Ser Ser Pro Ser Ala Phe Gln
20 25 30

Ala Val Thr Gly Phe Cys Arg Glu Gln Trp Gly Ile Pro Thr Val Phe
35 40 45

Cys Leu Gly Tyr Leu Ala Met Val Tyr Ala Ala Arg Arg Pro Leu Pro
50 55 60

Gln His Gly Tyr Met Val Ala Val Asp Arg Cys Phe Ala Ala Trp Asn
65 70 75 80

Leu Ala Leu Ser Val Phe Ser Thr Trp Gly Phe Tyr His Met Ala Val
85 90 95

79

Gly Leu Tyr Asn Met Thr Glu Thr Arg Gly Leu Gln Phe Thr Ile Cys
 100 105 110
 Gly Ser Thr Gly Glu Leu Val Gln Asn Leu Gln Thr Gly Pro Thr Ala
 115 120 125
 Leu Ala Leu Cys Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Met Asp
 130 135 140
 Thr Val Phe Leu Ile Leu Lys Ala Lys Lys Val Arg Phe Leu Gln Trp
 145 150 155 160
 Tyr His His Ala Thr Val Met Leu Phe Cys Trp Leu Ala Leu Ala Thr
 165 170 175
 Glu Tyr Thr Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His
 180 185 190
 Ser Ile Met Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Ser Ala Ala
 195 200 205
 Lys Val Val Lys Pro Ile Ala Pro Leu Ile Thr Val Ile Gln Ile Ala
 210 215 220
 Gln Met Val Trp Gly Leu Ile Val Asn Gly Ile Ala Ile Thr Thr Phe
 225 230 235 240
 Phe Thr Thr Gly Ala Cys Gln Ile Gln Ser Val Thr Val Tyr Ser Ala
 245 250 255
 Ile Ile Met Tyr Ala Ser Tyr Phe Tyr Leu Phe Ser Gln Leu Phe Phe
 260 265 270
 Glu Ala His Gly Ala Ala Gly Lys Asn Lys Lys Lys Leu Thr Arg Glu
 275 280 285
 Leu Ser Arg Lys Ile Ser Glu Ala Leu Leu Asn Thr Gly Asp Glu Val
 290 295 300
 Ser Lys His Leu Lys Val Asn
 305 310

<210> 49
 <211> 927
 <212> DNA
 <213> Crypthecodinium cohnii

<220>
 <221> CDS
 <222> (1) .. (927)
 <223> Delta-5-Elongase

<400> 49

atg gct tcc tac caa caa gca ttc tcc gaa ttg gct aga gct ttg tcc Met Ala Ser Tyr Gln Gln Ala Phe Ser Glu Leu Ala Arg Ala Leu Ser 1 5 10 15	48
act ttg aac cac gac ttc tcc agc gtc gag cca ttc aaa gtc gtg acg Thr Leu Asn His Asp Phe Ser Ser Val Glu Pro Phe Lys Val Val Thr 20 25 30	96
cag ttc tgc agg gac cag tgg gcg atc ccg aca gtc ttt tgc atc ggt Gln Phe Cys Arg Asp Gln Trp Ala Ile Pro Thr Val Phe Cys Ile Gly 35 40 45	144
tac ttg gca atg gtc tac gcc acg cga aga cct atc gcg aag cac ccc Tyr Leu Ala Met Val Tyr Ala Thr Arg Arg Pro Ile Ala Lys His Pro 50 55 60	192
tac atg tct ctc gtg gat cgc tgc ttt gcg gcc tgg aac ttg ggc ctc Tyr Met Ser Leu Val Asp Arg Cys Phe Ala Ala Trp Asn Leu Gly Leu 65 70 75 80	240
tcg ctc ttc agt tgc tgg ggc ttc tac cac atg gca gtg gga ctc tcc Ser Leu Phe Ser Cys Trp Gly Phe Tyr His Met Ala Val Gly Leu Ser 85 90 95	288
cac acc act tgg aat ttc ggg ctc cag ttc acc atc tgc ggc agc acc His Thr Thr Trp Asn Phe Gly Leu Gln Phe Thr Ile Cys Gly Ser Thr 100 105 110	336
acg gag ctt gtg aat ggc ttc cag aag ggc ccg gcg gcc ctc gcc ctc Thr Glu Leu Val Asn Gly Phe Gln Lys Gly Pro Ala Ala Leu Ala Leu 115 120 125	384
atc ctg ttc tgc ttc tcc aag atc ccg gag ttg ggc gac acc gtc ttc Ile Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Gly Asp Thr Val Phe 130 135 140	432
ttg atc ttg aag gga aag aag gtc cgc ttc ttg cag tgg tac cac cac Leu Ile Leu Lys Gly Lys Lys Val Arg Phe Leu Gln Trp Tyr His His 145 150 155 160	480
acg acc gtg atg ctc ttc tgt tgg atg gcc ttg gcg act gag tac act Thr Thr Val Met Leu Phe Cys Trp Met Ala Leu Ala Thr Glu Tyr Thr 165 170 175	528
cct gga ttg tgg ttc gcg gcc acg aac tac ttc gtg cac tcc atc atg Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His Ser Ile Met 180 185 190	576
tac atg tac ttc ttc ctc atg acc ttc aag acg gcc gcc ggc atc atc Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Thr Ala Ala Gly Ile Ile 195 200 205	624
aag ccc atc gcg cct ctc atc acc atc atc cag atc tcc cag atg gtc Lys Pro Ile Ala Pro Leu Ile Thr Ile Ile Gln Ile Ser Gln Met Val 210 215 220	672
tgg ggc ttg gtc gtg aac gcc atc gcc gtc ggc acc ttc ttc acc aca Trp Gly Leu Val Val Asn Ala Ile Ala Val Gly Thr Phe Phe Thr Thr 225 230 235 240	720
ggc aac tgc cag atc cag gca gtg aca gtc tac tcc gcc atc gtg atg Gly Asn Cys Gln Ile Gln Ala Val Thr Val Tyr Ser Ala Ile Val Met 245 250 255	768
tac gcc tcc tac ttc tac ctc ttc ggc cag ctc ttc ttc gag gcc cag Tyr Ala Ser Tyr Phe Tyr Leu Phe Gly Gln Leu Phe Phe Glu Ala Gln 260 265 270	816

ggt tcg gct gga aag gac aag aag aag ttg gcc cga gag ctg agc cga 864
 Gly Ser Ala Gly Lys Asp Lys Lys Lys Leu Ala Arg Glu Leu Ser Arg
 275 280 285

aag gtc tcg cgg gct ctc aca gca acg ggc gaa gag gtg tcg aag cac 912
 Lys Val Ser Arg Ala Leu Thr Ala Thr Gly Glu Glu Val Ser Lys His
 290 295 300

atg aag gtg aat tga 927
 Met Lys Val Asn
 305

<210> 50
 <211> 308
 <212> PRT
 <213> Crypthecodinium cohnii

<400> 50

Met Ala Ser Tyr Gln Gln Ala Phe Ser Glu Leu Ala Arg Ala Leu Ser
 1 5 10 15

Thr Leu Asn His Asp Phe Ser Ser Val Glu Pro Phe Lys Val Val Thr
 20 25 30

Gln Phe Cys Arg Asp Gln Trp Ala Ile Pro Thr Val Phe Cys Ile Gly
 35 40 45

Tyr Leu Ala Met Val Tyr Ala Thr Arg Arg Pro Ile Ala Lys His Pro
 50 55 60

Tyr Met Ser Leu Val Asp Arg Cys Phe Ala Ala Trp Asn Leu Gly Leu
 65 70 75 80

Ser Leu Phe Ser Cys Trp Gly Phe Tyr His Met Ala Val Gly Leu Ser
 85 90 95

His Thr Thr Trp Asn Phe Gly Leu Gln Phe Thr Ile Cys Gly Ser Thr
 100 105 110

Thr Glu Leu Val Asn Gly Phe Gln Lys Gly Pro Ala Ala Leu Ala Leu
 115 120 125

Ile Leu Phe Cys Phe Ser Lys Ile Pro Glu Leu Gly Asp Thr Val Phe
 130 135 140

Leu Ile Leu Lys Gly Lys Lys Val Arg Phe Leu Gln Trp Tyr His His
 145 150 155 160

Thr Thr Val Met Leu Phe Cys Trp Met Ala Leu Ala Thr Glu Tyr Thr
 165 170 175

Pro Gly Leu Trp Phe Ala Ala Thr Asn Tyr Phe Val His Ser Ile Met
 180 185 190

Tyr Met Tyr Phe Phe Leu Met Thr Phe Lys Thr Ala Ala Gly Ile Ile
195 200 205

Lys Pro Ile Ala Pro Leu Ile Thr Ile Ile Gln Ile Ser Gln Met Val
210 215 220

Trp Gly Leu Val Val Asn Ala Ile Ala Val Gly Thr Phe Phe Thr Thr
225 230 235 240

Gly Asn Cys Gln Ile Gln Ala Val Thr Val Tyr Ser Ala Ile Val Met
245 250 255

Tyr Ala Ser Tyr Phe Tyr Leu Phe Gly Gln Leu Phe Phe Glu Ala Gln
260 265 270

Gly Ser Ala Gly Lys Asp Lys Lys Lys Leu Ala Arg Glu Leu Ser Arg
275 280 285

Lys Val Ser Arg Ala Leu Thr Ala Thr Gly Glu Glu Val Ser Lys His
290 295 300

Met Lys Val Asn
305

<210> 51
<211> 795
<212> DNA
<213> Oncorhynchus mykiss

<220>
<221> CDS
<222> (1)..(795)
<223> Delta-5-Elongase

<400> 51
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Met Ala Ser Thr Trp Gln Ser Val Gln Ser Met Arg Gln Trp Ile Leu
1 5 10 15

gag aat gga gat aaa agg aca gac cca tgg cta ctg gtc tac tcc cct 96
Glu Asn Gly Asp Lys Arg Thr Asp Pro Trp Leu Leu Val Tyr Ser Pro
20 25 30

atg cca gtg gcc att ata ttc ctc ctc tat ctt ggt gtg gtc tgg gct 144
Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala
35 40 45

ggg ccc aag ctg atg aaa cgc agg gaa cca gtt gat ctc aag gct gta 192
Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val
50 55 60

ctc att gtc tac aac ttc gcc atg gtc tgc ctg tct gtc tac atg ttc 240
Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe
65 70 75 80

cat gag ttc ttg gtc acg tcc ttg ctg tct aac tac agt tac ctg tgt 288
His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys
85 90 95

83

caa cct gtg gat tac agc act agt cca ctg gcg atg agg atg gcc aaa 336
 Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys
 100 105 110

gta tgc tgg tgg ttt ttc ttc tcc aag gtc ata gaa ttg gct gac acg 384
 Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr
 115 120 125

gtg ttc ttc atc ctg agg aag aag aac agt cag ctg act ttc ctg cat 432
 Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His
 130 135 140

gtc tat cac cat ggc acc atg atc ttc aac tgg tgg gca ggg gtc aag 480
 Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys
 145 150 155 160

tat ctg gct gga ggc caa tgc ttc ttc atc ggc ctg ctc aat acc ttt 528
 Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe
 165 170 175

gtg cac atc gtg atg tac tct tac tac gga ctg gct gcc ctg ggg cct 576
 Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro
 180 185 190

cac acg cag aag tac tta tgg tgg aag cgc tat ctg acc tca ctg cag 624
 His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln
 195 200 205

ctg ctc cag ttt gtc ctg ttg acc act cac act ggc tac aac ctc ttc 672
 Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe
 210 215 220

act gag tgt gac ttc ccg gac tcc atg aac gct gtg gtg ttt gcc tac 720
 Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr
 225 230 235 240

tgt gtc agt ctc att gct ctc ttc agc aac ttc tac tat cag agc tac 768
 Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr
 245 250 255

ctc aac agg aag agc aag aag aca taa 795
 Leu Asn Arg Lys Ser Lys Lys Thr
 260

<210> 52
 <211> 264
 <212> PRT
 <213> Oncorhynchus mykiss

<400> 52

Met Ala Ser Thr Trp Gln Ser Val Gln Ser Met Arg Gln Trp Ile Leu
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Glu Asn Gly Asp Lys Arg Thr Asp Pro Trp Leu Leu Val Tyr Ser Pro
 20 25 30

Met Pro Val Ala Ile Ile Phe Leu Leu Tyr Leu Gly Val Val Trp Ala
 35 40 45

Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val
 50 55 60

84

Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe
65 70 75 80

His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys
85 90 95

Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys
100 105 110

Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr
115 120 125

Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His
130 135 140

Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys
145 150 155 160

Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe
165 170 175

Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro
180 185 190

His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln
195 200 205

Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe
210 215 220

Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr
225 230 235 240

Cys Val Ser Leu Ile Ala Leu Phe Ser Asn Phe Tyr Tyr Gln Ser Tyr
245 250 255

Leu Asn Arg Lys Ser Lys Lys Thr
260

<210> 53
<211> 885
<212> DNA
<213> Oncorhynchus mykiss

<220>
<221> CDS
<222> (1)..(885)
<223> Delta-5-Elongase

<400> 53
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Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met
1 5 10 15

ggt ccc aga gat gag cgg gta cag gga tgg ctg ctt ctg gac aac tac Gly Pro Arg Asp Glu Arg Val Gln Gly Trp Leu Leu Leu Asp Asn Tyr 20 25 30	96
cct cca acc ttt gca cta aca gtc atg tac ctg ctg atc gta tgg atg Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met 35 40 45	144
ggg ccc aag tac atg aga cac aga cag ccg gtg tct tgc cgg ggt ctc Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu 50 55 60	192
ctc ttg gtc tac aat ctg ggc ctc acg atc ttg tcc ttc tat atg ttc Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe 65 70 75 80	240
tat gag atg gtg tct gct gtg tgg cac ggg gat tat aac ttc ttt tgc Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys 85 90 95	288
caa gac aca cac agt gca gga gaa acc gat acc aag atc ata aat gtg Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val 100 105 110	336
ctg tgg tgg tac tac ttc tcc aag ctc ata gag ttt atg gat acc ttc Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe 115 120 125	384
ttc ttc atc ctg cgg aag aac aac cat caa atc acg ttt ctg cac atc Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile 130 135 140	432
tac cac cat gct agc atg ctc aac atc tgg tgg ttc gtc atg aac tgg Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp 145 150 155 160	480
gtg ccc tgt ggt cac tcc tac ttt ggt gcc tcc ctg aac agc ttc atc Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile 165 170 175	528
cat gtc ctg atg tac tct tac tat ggg ctc tct gct gtc ccg gcc ttg His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu 180 185 190	576
cgg ccc tat cta tgg tgg aag aaa tac atc aca caa gta cag ctg att Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile 195 200 205	624
cag ttc ttt ttg acc atg tcc cag acg ata tgt gca gtc att tgg cca Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro 210 215 220	672
tgt gat ttc ccc aga ggg tgg ctg tat ttc cag ata ttc tat gtc atc Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile 225 230 235 240	720
aca ctt att gcc ctt ttc tca aac ttc tac att cag act tac aag aaa Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys 245 250 255	768
cac ctt gtt tca caa aag aag gag tat cat cag aat ggc tct gtt gct His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala 260 265 270	816
tca ttg aat ggc cat gtg aat ggg gtg aca ccc acg gaa acc att aca Ser Leu Asn Gly His Val Asn Gly Val Thr Pro Thr Glu Thr Ile Thr 275 280 285	864

cac agg aaa gtg agg ggg gac
 His Arg Lys Val Arg Gly Asp
 290 295

<210> 54
 <211> 295
 <212> PRT
 <213> Oncorhynchus mykiss

<400> 54

Met Glu Thr Phe Asn Tyr Lys Leu Asn Met Tyr Ile Asp Ser Trp Met
 1 5 10 15

Gly Pro Arg Asp Glu Arg Val Gln Gly Trp Leu Leu Leu Asp Asn Tyr
 20 25 30

Pro Pro Thr Phe Ala Leu Thr Val Met Tyr Leu Leu Ile Val Trp Met
 35 40 45

Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu
 50 55 60

Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe
 65 70 75 80

Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys
 85 90 95

Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val
 100 105 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
 115 120 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile
 130 135 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
 145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile
 165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu
 180 185 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile
 195 200 205

Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro
 210 215 220

Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile
 225 230 235 240

Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys
 245 250 255

His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala
 260 265 270

Ser Leu Asn Gly His Val Asn Gly Val Thr Pro Thr Glu Thr Ile Thr
 275 280 285

His Arg Lys Val Arg Gly Asp
 290 295

<210> 55
 <211> 6753
 <212> DNA
 <213> Oncorhynchus mykiss

<220>
 <221> CDS
 <222> (513)..(1397)
 <223> Delta-5-Elongase

<400> 55
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 acaataaaga ttctacaata ctagctttta tggttatgaa gaggaaaaat tggcagtaac 180
 ctggccccac aaaccttcaa atgaacgaat caaattaaca accataggat gataatgcga 240
 ttagtttttt agccttattt ctggggtaat taatcagcga agcgatgatt tttgatctat 300
 taacagatat ataaatgcaa aaactgcatt aaccacttta actaatactt tcaacatttt 360
 cggtttgtat tacttcttat tcaaagttaa taaaagtatc aacaaaaaat tgttaatata 420
 cctctatact ttaacgtcaa ggagaaaaaa ccccgatcg gactactagc agctgtaata 480
 cgactcacta tagggaatat taagcttaca ta atg gag act ttt aat tat aaa 533
 Met Glu Thr Phe Asn Tyr Lys
 1 5
 cta aac atg tac ata gac tca tgg atg ggt ccc aga gat gag cgg gta 581
 Leu Asn Met Tyr Ile Asp Ser Trp Met Gly Pro Arg Asp Glu Arg Val
 10 15 20
 cag gga tgg ctg ctt ctg gac aac tac cct cca acc ttt gca cta aca 629
 Gln Gly Trp Leu Leu Leu Asp Asn Tyr Pro Pro Thr Phe Ala Leu Thr
 25 30 35
 gtc atg tac ctg ctg atc gta tgg atg ggg ccc aag tac atg aga cac 677
 Val Met Tyr Leu Leu Ile Val Trp Met Gly Pro Lys Tyr Met Arg His
 40 45 50 55
 aga cag ccg gtg tct tgc cgg ggt ctc ctc ttg gtc tac aat ctg ggc 725
 Arg Gln Pro Val Ser Cys Arg Gly Leu Leu Leu Val Tyr Asn Leu Gly
 60 65 70

ctc acg atc ttg tcc ttc tat atg ttc tat gag atg gtg tct gct gtg Leu Thr Ile Leu Ser Phe Tyr Met Phe Tyr Glu Met Val Ser Ala Val	773
75 80 85	
tgg cac ggg gat tat aac ttc ttt tgc caa gac aca cac agt gca gga Trp His Gly Asp Tyr Asn Phe Phe Cys Gln Asp Thr His Ser Ala Gly	821
90 95 100	
gaa acc gat acc aag atc ata aat gtg ctg tgg tgg tac tac ttc tcc Glu Thr Asp Thr Lys Ile Ile Asn Val Leu Trp Trp Tyr Tyr Phe Ser	869
105 110 115	
aag ctc ata gag ttt atg gat acc ttc ttc ttc atc ctg cgg aag aac Lys Leu Ile Glu Phe Met Asp Thr Phe Phe Phe Ile Leu Arg Lys Asn	917
120 125 130 135	
aac cat caa atc acg ttt ctg cac atc tac cac cat gct agc atg ctc Asn His Gln Ile Thr Phe Leu His Ile Tyr His His Ala Ser Met Leu	965
140 145 150	
aac atc tgg tgg ttc gtc atg aac tgg gtg ccc tgt ggt cac tcc tac Asn Ile Trp Trp Phe Val Met Asn Trp Val Pro Cys Gly His Ser Tyr	1013
155 160 165	
ttt ggt gcc tcc ctg aac agc ttc atc cat gtc ctg atg tac tct tac Phe Gly Ala Ser Leu Asn Ser Phe Ile His Val Leu Met Tyr Ser Tyr	1061
170 175 180	
tat ggg ctc tct gct gtc ccg gcc ttg cgg ccc tat cta tgg tgg aag Tyr Gly Leu Ser Ala Val Pro Ala Leu Arg Pro Tyr Leu Trp Trp Lys	1109
185 190 195	
aaa tac atc aca caa gta cag ctg att cag ttc ttt ttg acc atg tcc Lys Tyr Ile Thr Gln Val Gln Leu Ile Gln Phe Phe Leu Thr Met Ser	1157
200 205 210 215	
cag acg ata tgt gca gtc att tgg cca tgt gat ttc ccc aga ggg tgg Gln Thr Ile Cys Ala Val Ile Trp Pro Cys Asp Phe Pro Arg Gly Trp	1205
220 225 230	
ctg tat ttc cag ata ttc tat gtc atc aca ctt att gcc ctt ttc tca Leu Tyr Phe Gln Ile Phe Tyr Val Ile Thr Leu Ile Ala Leu Phe Ser	1253
235 240 245	
aac ttc tac att cag act tac aag aaa cac ctt gtt tca caa aag aag Asn Phe Tyr Ile Gln Thr Tyr Lys Lys His Leu Val Ser Gln Lys Lys	1301
250 255 260	
gag tat cat cag aat ggc tct gtt gct tca ttg aat ggc cat gtg aat Glu Tyr His Gln Asn Gly Ser Val Ala Ser Leu Asn Gly His Val Asn	1349
265 270 275	
ggg gtg aca ccc acg gaa acc att aca cac agg aaa gtg agg ggg gac Gly Val Thr Pro Thr Glu Thr Ile Thr His Arg Lys Val Arg Gly Asp	1397
280 285 290 295	
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ggcggccgct cgagtctaga gggcccttcg aaggtaagcc tatccctaac cctctcctcg	1517
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35 40 45

Gly Pro Lys Tyr Met Arg His Arg Gln Pro Val Ser Cys Arg Gly Leu
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Leu Leu Val Tyr Asn Leu Gly Leu Thr Ile Leu Ser Phe Tyr Met Phe
65 70 75 80

Tyr Glu Met Val Ser Ala Val Trp His Gly Asp Tyr Asn Phe Phe Cys
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Gln Asp Thr His Ser Ala Gly Glu Thr Asp Thr Lys Ile Ile Asn Val
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Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Phe Leu His Ile
 130 135 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
 145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Ser Leu Asn Ser Phe Ile
 165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ala Val Pro Ala Leu
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Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Val Gln Leu Ile
 195 200 205

Gln Phe Phe Leu Thr Met Ser Gln Thr Ile Cys Ala Val Ile Trp Pro
 210 215 220

Cys Asp Phe Pro Arg Gly Trp Leu Tyr Phe Gln Ile Phe Tyr Val Ile
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Thr Leu Ile Ala Leu Phe Ser Asn Phe Tyr Ile Gln Thr Tyr Lys Lys
 245 250 255

His Leu Val Ser Gln Lys Lys Glu Tyr His Gln Asn Gly Ser Val Ala
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His Arg Lys Val Arg Gly Asp
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Asp Pro Trp Leu Leu Val Tyr Ser Pro Met Pro Val Ala Ile Ile Phe	
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Met Val Cys Leu Ser Val Tyr Met Phe His Glu Phe Leu Val Thr Ser	
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Ser Pro Leu Ala Met Arg Met Ala Lys Val Cys Trp Trp Phe Phe Phe	
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Ser Lys Val Ile Glu Leu Ala Asp Thr Val Phe Phe Ile Leu Arg Lys	
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 <213> *Oncorhynchus mykiss*

<400> 58

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 35 40 45

Gly Pro Lys Leu Met Lys Arg Arg Glu Pro Val Asp Leu Lys Ala Val
 50 55 60

Leu Ile Val Tyr Asn Phe Ala Met Val Cys Leu Ser Val Tyr Met Phe
 65 70 75 80

His Glu Phe Leu Val Thr Ser Leu Leu Ser Asn Tyr Ser Tyr Leu Cys
 85 90 95

Gln Pro Val Asp Tyr Ser Thr Ser Pro Leu Ala Met Arg Met Ala Lys
 100 105 110

Val Cys Trp Trp Phe Phe Phe Ser Lys Val Ile Glu Leu Ala Asp Thr
 115 120 125

Val Phe Phe Ile Leu Arg Lys Lys Asn Ser Gln Leu Thr Phe Leu His
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Val Tyr His His Gly Thr Met Ile Phe Asn Trp Trp Ala Gly Val Lys
 145 150 155 160

Tyr Leu Ala Gly Gly Gln Ser Phe Phe Ile Gly Leu Leu Asn Thr Phe
 165 170 175

Val His Ile Val Met Tyr Ser Tyr Tyr Gly Leu Ala Ala Leu Gly Pro
 180 185 190

His Thr Gln Lys Tyr Leu Trp Trp Lys Arg Tyr Leu Thr Ser Leu Gln
 195 200 205

Leu Leu Gln Phe Val Leu Leu Thr Thr His Thr Gly Tyr Asn Leu Phe
 210 215 220

Thr Glu Cys Asp Phe Pro Asp Ser Met Asn Ala Val Val Phe Ala Tyr
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Leu Asn Arg Lys Ser Lys Lys Thr
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<213> *Thalassiosira pseudonana*

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 His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu
 35 40 45
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 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu
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 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val
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 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
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 gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 384
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly
 115 120 125
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 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys
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 gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg 480
 Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly
 145 150 155 160
 aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata 528
 Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile
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355																				

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<211> 358

<212> PRT

<213> Thalassiosira pseudonana

<400> 60

Met	Cys	Ser	Ser	Pro	Pro	Ser	Gln	Ser	Lys	Thr	Thr	Ser	Leu	Leu	Ala
1				5					10					15	

Arg	Tyr	Thr	Thr	Ala	Ala	Leu	Leu	Leu	Leu	Thr	Leu	Thr	Thr	Trp	Cys
			20					25					30		

His	Phe	Ala	Phe	Pro	Ala	Ala	Thr	Ala	Thr	Pro	Gly	Leu	Thr	Ala	Glu
		35					40					45			

Met	His	Ser	Tyr	Lys	Val	Pro	Leu	Gly	Leu	Thr	Val	Phe	Tyr	Leu	Leu
	50					55					60				

Ser	Leu	Pro	Ser	Leu	Lys	Tyr	Val	Thr	Asp	Asn	Tyr	Leu	Ala	Lys	Lys
65					70					75					80

Tyr	Asp	Met	Lys	Ser	Leu	Leu	Thr	Glu	Ser	Met	Val	Leu	Tyr	Asn	Val
				85					90					95	

Ala	Gln	Val	Leu	Leu	Asn	Gly	Trp	Thr	Val	Tyr	Ala	Ile	Val	Asp	Ala
			100					105					110		

Val	Met	Asn	Arg	Asp	His	Pro	Phe	Ile	Gly	Ser	Arg	Ser	Leu	Val	Gly
		115					120					125			

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys
 130 135 140

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly
 145 150 155 160

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile
 165 170 175

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile
 180 185 190

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser
 195 200 205

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr
 210 215 220

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr
 225 230 235 240

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp
 245 250 255

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln
 260 265 270

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys
 275 280 285

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys
 290 295 300

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp
 305 310 315 320

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala
 325 330 335

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr
 340 345 350

Arg Val Thr Gly Ala Met
 355

<210> 61

<211> 933

<212> DNA

<213> Thalassiosira pseudonana

<220>

<221> CDS
 <222> (1)..(933)
 <223> Delta-5-Elongase

<400> 61
 atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 48
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu
 1 5 10 15
 agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag 96
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys
 20 25 30
 tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg 144
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val
 35 40 45
 gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg 192
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
 50 55 60
 gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 240
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly
 65 70 75 80
 gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt 288
 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys
 85 90 95
 gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg 336
 Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly
 100 105 110
 aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata 384
 Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile
 115 120 125
 gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att 432
 Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile
 130 135 140
 tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc 480
 Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser
 145 150 155 160
 tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac 528
 Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr
 165 170 175
 ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg 576
 Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr
 180 185 190
 ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat 624
 Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp
 195 200 205
 gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag 672
 Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln
 210 215 220
 gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa 720
 Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys
 225 230 235 240
 cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag 768
 Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys

102

245	250	255	
aat gat gat ggg aat aat gag gat	caa tgt cac aag gct atg aag gat		816
Asn Asp Asp Gly Asn Asn Glu Asp	Gln Cys His Lys Ala Met Lys Asp		
260	265	270	
ata tcg gag ggt gcg aag gag gtt	gtg ggg cat gca gcg aag gat gct		864
Ile Ser Glu Gly Ala Lys Glu Val	Val Gly His Ala Ala Lys Asp Ala		
275	280	285	
gga aag ttg gtg gct acg gcg agt	aag gct gta aag agg aag gga act		912
Gly Lys Leu Val Ala Thr Ala Ser	Lys Ala Val Lys Arg Lys Gly Thr		
290	295	300	
cgt gtt act ggt gcc atg tag			933
Arg Val Thr Gly Ala Met			
305	310		

<210> 62
 <211> 310
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 62

Met His Ser Tyr Lys Val Pro Leu Gly	Leu Thr Val Phe Tyr Leu Leu	
1	5	10
Ser Leu Pro Ser Leu Lys Tyr Val Thr	Asp Asn Tyr Leu Ala Lys Lys	
20	25	30
Tyr Asp Met Lys Ser Leu Leu Thr Glu	Ser Met Val Leu Tyr Asn Val	
35	40	45
Ala Gln Val Leu Leu Asn Gly Trp Thr	Val Tyr Ala Ile Val Asp Ala	
50	55	60
Val Met Asn Arg Asp His Pro Phe Ile	Gly Ser Arg Ser Leu Val Gly	
65	70	75
Ala Ala Leu His Ser Gly Ser Ser Tyr	Ala Val Trp Val His Tyr Cys	
85	90	95
Asp Lys Tyr Leu Glu Phe Phe Asp Thr	Tyr Phe Met Val Leu Arg Gly	
100	105	110
Lys Met Asp Gln Val Ser Phe Leu His	Ile Tyr His His Thr Thr Ile	
115	120	125
Ala Trp Ala Trp Trp Ile Ala Leu Arg	Phe Ser Pro Gly Gly Asp Ile	
130	135	140
Tyr Phe Gly Ala Leu Leu Asn Ser Ile	Ile His Val Leu Met Tyr Ser	
145	150	155
Tyr Tyr Ala Leu Ala Leu Leu Lys Val	Ser Cys Pro Trp Lys Arg Tyr	
165	170	175

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr
 180 185 190

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp
 195 200 205

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln
 210 215 220

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys
 225 230 235 240

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys
 245 250 255

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp
 260 265 270

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala
 275 280 285

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr
 290 295 300

Arg Val Thr Gly Ala Met
 305 310

<210> 63
 <211> 933
 <212> DNA
 <213> Thalassiosira pseudonana

<220>
 <221> CDS
 <222> (1)..(933)
 <223> Delta-5-Elongase

<400> 63
 atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 48
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu
 1 5 10 15

agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag 96
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys
 20 25 30

tat gat atg aag tca ctc cta acg gaa tca atg gtg ttg tac aat gtg 144
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val
 35 40 45

gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg 192
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
 50 55 60

gtg atg aat aga gac cat ccg ttt att gga agt aga agt ttg gtt ggg 240
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly

104

65	70	75	80	
gcg gcg ttg cat agt ggg agc tcg tat	gcg gtg tgg gtt cat tat tgt			288
Ala Ala Leu His Ser Gly Ser Ser Tyr	Ala Val Trp Val His Tyr Cys			
85	90		95	
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg				336
Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly				
100	105		110	
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata				384
Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile				
115	120		125	
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggt gga gac att				432
Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile				
130	135		140	
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc				480
Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser				
145	150		155	160
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac				528
Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr				
165	170		175	
ctg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg				576
Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr				
180	185		190	
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat				624
Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp				
195	200		205	
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag				672
Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln				
210	215		220	
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa				720
Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys				
225	230		235	240
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag				768
Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys				
245	250		255	
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat				816
Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp				
260	265		270	
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct				864
Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala				
275	280		285	
gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act				912
Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr				
290	295		300	
cgt gtt act ggt gcc atg tag				933
Arg Val Thr Gly Ala Met				
305	310			

<210> 64

<211> 310

<212> PRT

<213> Thalassiosira pseudonana

<400> 64

Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu
1 5 10 15

Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys
20 25 30

Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val
35 40 45

Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
50 55 60

Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly
65 70 75 80

Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys
85 90 95

Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly
100 105 110

Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile
115 120 125

Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile
130 135 140

Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser
145 150 155 160

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr
165 170 175

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr
180 185 190

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp
195 200 205

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln
210 215 220

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys
225 230 235 240

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys
245 250 255

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp
260 265 270

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala
275 280 285

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr
290 295 300

Arg Val Thr Gly Ala Met
305 310

<210> 65
<211> 825
<212> DNA
<213> *Thraustochytrium aureum*

<220>
<221> CDS
<222> (1)..(825)
<223> Delta-5-Elongase

<400> 65
atg acg agc aac atg agc gcg tgg ggc gtc gcc gtc gac cag acg cag 48
Met Thr Ser Asn Met Ser Ala Trp Gly Val Ala Val Asp Gln Thr Gln
1 5 10 15
cag gtc gtc gac cag atc atg ggc ggc gcc gag ccg tac aag ctg aca 96
Gln Val Val Asp Gln Ile Met Gly Gly Ala Glu Pro Tyr Lys Leu Thr
20 25 30
gaa ggg cgc atg acg aac gtc gag acg atg ctg gcg atc gag tgc ggc 144
Glu Gly Arg Met Thr Asn Val Glu Thr Met Leu Ala Ile Glu Cys Gly
35 40 45
tac gcc gcc atg ctg ctg ttc ctg acc ccg atc atg aag cag gcc gag 192
Tyr Ala Ala Met Leu Leu Phe Leu Thr Pro Ile Met Lys Gln Ala Glu
50 55 60
aag ccc ttc gag ctc aag tcc ttc aag ctc gcc cac aac ctg ttc ctg 240
Lys Pro Phe Glu Leu Lys Ser Phe Lys Leu Ala His Asn Leu Phe Leu
65 70 75 80
ttc gtc ctg tcc gcc tac atg tgc ctc gag acc gtc cgc cag gcc tac 288
Phe Val Leu Ser Ala Tyr Met Cys Leu Glu Thr Val Arg Gln Ala Tyr
85 90 95
ctt gcg ggc tac tcg gtg ttc ggc aac gac atg gag aag ggc agc gag 336
Leu Ala Gly Tyr Ser Val Phe Gly Asn Asp Met Glu Lys Gly Ser Glu
100 105 110
ccg cac gcg cac ggc atg gcc caa atc gtg tgg atc ttt tac gtg tcc 384
Pro His Ala His Gly Met Ala Gln Ile Val Trp Ile Phe Tyr Val Ser
115 120 125
aag gcg tac gag ttc gtg gac acg ctg atc atg atc ctg tgc aaa aag 432
Lys Ala Tyr Glu Phe Val Asp Thr Leu Ile Met Ile Leu Cys Lys Lys
130 135 140
ttc aac cag gtc tcc gtc ctg cac gtg tac cac cac gcc acc atc ttt 480
Phe Asn Gln Val Ser Val Leu His Val Tyr His His Ala Thr Ile Phe
145 150 155 160
gct atc tgg ttt atg atc gcc aag tac gcc ccg ggc ggc gac gca tac 528
Ala Ile Trp Phe Met Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr

107

165	170	175	
ttt agc gtc atc ctg aac tcg ttc gtg cac acc gtc atg tac gcg tac			576
Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr			
180	185	190	
tac ttc ttc tcg tcg cag ggc ttc ggg ttc gtc aag ccg atc aag ccg			624
Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro			
195	200	205	
tac atc acc tcg ctg cag atg acg cag ttc atg gcg atg ctc gtg cag			672
Tyr Ile Thr Ser Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln			
210	215	220	
tcg ctg tac gac tac ctt tac ccg tgc gac tac ccg cag ggg ctc gtc			720
Ser Leu Tyr Asp Tyr Leu Tyr Pro Cys Asp Tyr Pro Gln Gly Leu Val			
225	230	235	240
aag ctc ctc ggc gtg tac atg ctc acc ctg ctt gcg ctc ttc ggc aac			768
Lys Leu Leu Gly Val Tyr Met Leu Thr Leu Leu Ala Leu Phe Gly Asn			
245	250	255	
ttt ttc gtg cag agc tac ctc aag aag tcg aac aag ccc aag gcc aag			816
Phe Phe Val Gln Ser Tyr Leu Lys Lys Ser Asn Lys Pro Lys Ala Lys			
260	265	270	
tcg gcc taa			825
Ser Ala			

<210> 66
 <211> 274
 <212> PRT
 <213> Thraustochytrium aureum

<400> 66

Met Thr Ser Asn Met Ser Ala Trp Gly Val Ala Val Asp Gln Thr Gln
1 5 10 15

Gln Val Val Asp Gln Ile Met Gly Gly Ala Glu Pro Tyr Lys Leu Thr
20 25 30

Glu Gly Arg Met Thr Asn Val Glu Thr Met Leu Ala Ile Glu Cys Gly
35 40 45

Tyr Ala Ala Met Leu Leu Phe Leu Thr Pro Ile Met Lys Gln Ala Glu
50 55 60

Lys Pro Phe Glu Leu Lys Ser Phe Lys Leu Ala His Asn Leu Phe Leu
65 70 75 80

Phe Val Leu Ser Ala Tyr Met Cys Leu Glu Thr Val Arg Gln Ala Tyr
85 90 95

Leu Ala Gly Tyr Ser Val Phe Gly Asn Asp Met Glu Lys Gly Ser Glu
100 105 110

Pro His Ala His Gly Met Ala Gln Ile Val Trp Ile Phe Tyr Val Ser
115 120 125

Lys Ala Tyr Glu Phe Val Asp Thr Leu Ile Met Ile Leu Cys Lys Lys
130 135 140

Phe Asn Gln Val Ser Val Leu His Val Tyr His His Ala Thr Ile Phe
145 150 155 160

Ala Ile Trp Phe Met Ile Ala Lys Tyr Ala Pro Gly Gly Asp Ala Tyr
165 170 175

Phe Ser Val Ile Leu Asn Ser Phe Val His Thr Val Met Tyr Ala Tyr
180 185 190

Tyr Phe Phe Ser Ser Gln Gly Phe Gly Phe Val Lys Pro Ile Lys Pro
195 200 205

Tyr Ile Thr Ser Leu Gln Met Thr Gln Phe Met Ala Met Leu Val Gln
210 215 220

Ser Leu Tyr Asp Tyr Leu Tyr Pro Cys Asp Tyr Pro Gln Gly Leu Val
225 230 235 240

Lys Leu Leu Gly Val Tyr Met Leu Thr Leu Leu Ala Leu Phe Gly Asn
245 250 255

Phe Phe Val Gln Ser Tyr Leu Lys Lys Ser Asn Lys Pro Lys Ala Lys
260 265 270

Ser Ala

<210> 67
<211> 903
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(903)
<223> Delta-5-Elongase

<400> 67
atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly

50	55	60	
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met 65 70 75 80			240
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly 85 90 95			288
atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser 100 105 110			336
acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val 115 120 125			384
tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe 130 135 140			432
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr 145 150 155 160			480
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met 165 170 175			528
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser 180 185 190			576
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly 195 200 205			624
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln 210 215 220			672
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His 225 230 235 240			720
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met 245 250 255			768
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser 260 265 270			816
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala 275 280 285			864
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp 290 295 300			903

<210> 68

<211> 300

<212> PRT

<213> *Ostreococcus tauri*

<400> 68

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
1 5 10 15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
20 25 30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
35 40 45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
50 55 60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65 70 75 80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
85 90 95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
115 120 125

Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
 290 295 300

<210> 69
 <211> 879
 <212> DNA
 <213> *Ostreococcus tauri*

<220>
 <221> CDS
 <222> (1)..(879)
 <223> Delta-6-Elongase

<400> 69
 atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48
 Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
 1 5 10 15
 tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96
 Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
 20 25 30
 cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144
 Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
 35 40 45
 att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc 192
 Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
 50 55 60
 aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa 240
 Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
 65 70 75 80
 att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg 288
 Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
 85 90 95
 ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa 336
 Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
 100 105 110
 gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg 384
 Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
 115 120 125
 gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata 432
 Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
 130 135 140
 tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg 480
 Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
 145 150 155 160
 caa gta agt ttc cta cac att tat cac cac agc acg att tcc ttt att 528
 Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile
 165 170 175
 tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc 576
 Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser

180	185	190	
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta			624
Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu			
195	200	205	
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt			672
Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu			
210	215	220	
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc			720
Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe			
225	230	235	240
aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag			768
Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys			
245	250	255	
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg			816
Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu			
260	265	270	
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag			864
Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln			
275	280	285	
aaa aaa cag cag tga			879
Lys Lys Gln Gln			
290			

<210> 70
 <211> 292
 <212> PRT
 <213> *Ostreococcus tauri*

<400> 70

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
115 120 125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
 130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
 145 150 155 160

Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile
 165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
 180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
 195 200 205

Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu
 210 215 220

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
 225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
 245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
 260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
 275 280 285

Lys Lys Gln Gln
 290

<210> 71
 <211> 1362
 <212> DNA
 <213> *Primula farinosa*

<220>
 <221> CDS
 <222> (1)..(1362)
 <223> Delta-6-Desaturase

<400> 71
 atg gct aac aaa tct cca cca aac ccc aaa aca ggt tac ata acc agc 48
 Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser
 1 5 10 15
 tca gac ctg aaa tcc cac aac aag gca ggt gac cta tgg ata tca atc 96
 Ser Asp Leu Lys Ser His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile
 20 25 30
 cac ggc caa gtc tac gac gtg tcc tct tgg gcc gcc ctt cat ccg ggg 144
 His Gly Gln Val Tyr Asp Val Ser Ser Trp Ala Ala Leu His Pro Gly

35	40	45	
ggc act gcc cct ctc atg gcc ctt gca gga cac gac gtg acc gat gct Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala 50 55 60			192
ttc ctc gcg tac cat ccc cct tcc act gcc cgt ctc ctc cct cct ctc Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu 65 70 75 80			240
tct acc aac ctc ctt ctt caa aac cac tcc gtc tcc ccc acc tcc tca Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser 85 90 95			288
gac tac cgc aaa ctc ctc gac aac ttc cat aaa cat gcc ctt ttc cgc Asp Tyr Arg Lys Leu Leu Asp Asn Phe His Lys His Gly Leu Phe Arg 100 105 110			336
gcc agg gcc cac act gct tac gcc acc ttc gtc ttc atg ata gcg atg Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Phe Met Ile Ala Met 115 120 125			384
ttt cta atg agc gtg act gga gtc ctt tgc agc gac agt gcg tgg gtc Phe Leu Met Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val 130 135 140			432
cat ttg gct agc gcc gga gca atg ggg ttc gcc tgg atc caa tgc gga His Leu Ala Ser Gly Gly Ala Met Gly Phe Ala Trp Ile Gln Cys Gly 145 150 155 160			480
tgg ata ggt cac gac tct ggg cat tac cgg att atg tct gac agg aaa Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys 165 170 175			528
tgg aac tgg ttc gcg caa atc cta agc aca aac tgc ctc cag ggg att Trp Asn Trp Phe Ala Gln Ile Leu Ser Thr Asn Cys Leu Gln Gly Ile 180 185 190			576
agt atc ggg tgg tgg aag tgg aac cat aat gcg cac cac atc gct tgc Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys 195 200 205			624
aat agc ctg gat tac gac ccc gac ctc cag tat atc cct ttg ctc gtc Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val 210 215 220			672
gtc tcc ccc aag ttc ttc aac tcc ctt act tct cgt ttc tac gac aag Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys 225 230 235 240			720
aag ctg aac ttc gac gcc gtg tcg agg ttt ctg gtt tgc tac cag cac Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His 245 250 255			768
tgg acg ttt tat ccg gtc atg tgt gtc gct agg ctg aac atg ctc gcg Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Leu Ala 260 265 270			816
cag tca ttt ata acg ctt ttc tcg agt agg gag gtg tgc cat agg gcg Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Cys His Arg Ala 275 280 285			864
caa gag gtt ttc gga ctt gcc gtg ttt tgg gtt tgg ttt ccg ctt tta Gln Glu Val Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu 290 295 300			912
ctt tct tgt tta cct aat tgg gcc gag agg att atg ttt ttg ctt gcg Leu Ser Cys Leu Pro Asn Trp Gly Glu Arg Ile Met Phe Leu Leu Ala			960

115

305	310	315	320	
agc tat tcc gtt acg ggg ata caa cac gtg cag ttc agc ttg aac cat				1008
Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His				
325		330	335	
ttt tct tcg gac gtc tat gtg ggc ccg cca gta ggt aat gac tgg ttc				1056
Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Gly Asn Asp Trp Phe				
340		345	350	
aag aaa cag act gcc ggg aca ctt aac ata tcg tgc ccg gcg tgg atg				1104
Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met				
355		360	365	
gat tgg ttc cat ggc ggg tta cag ttt cag gtc gag cac cac ttg ttt				1152
Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe				
370		375	380	
ccg cgg atg cct agg ggt cag ttt agg aag att tct cct ttt gtg agg				1200
Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg				
385		390	395	400
gat ttg tgt aag aaa cac aac ttg cct tac aat atc gcg tct ttt act				1248
Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr				
405		410	415	
aaa gcg aat gtg ttt acg ctt aag acg ctg aga aat acg gcc att gag				1296
Lys Ala Asn Val Phe Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu				
420		425	430	
gct cgg gac ctc tct aat ccg ctc cca aag aat atg gtg tgg gaa gct				1344
Ala Arg Asp Leu Ser Asn Pro Leu Pro Lys Asn Met Val Trp Glu Ala				
435		440	445	
ctt aaa act ctc ggg tga				1362
Leu Lys Thr Leu Gly				
450				

<210> 72
 <211> 453
 <212> PRT
 <213> Primula farinosa

<400> 72

Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser			
1	5	10	15
Ser Asp Leu Lys Ser His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile			
20	25	30	
His Gly Gln Val Tyr Asp Val Ser Ser Trp Ala Ala Leu His Pro Gly			
35	40	45	
Gly Thr Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala			
50	55	60	
Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu			
65	70	75	80
Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser			
85	90	95	

Asp Tyr Arg Lys Leu Leu Asp Asn Phe His Lys His Gly Leu Phe Arg
 100 105 110

Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Phe Met Ile Ala Met
 115 120 125

Phe Leu Met Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val
 130 135 140

His Leu Ala Ser Gly Gly Ala Met Gly Phe Ala Trp Ile Gln Cys Gly
 145 150 155 160

Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys
 165 170 175

Trp Asn Trp Phe Ala Gln Ile Leu Ser Thr Asn Cys Leu Gln Gly Ile
 180 185 190

Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys
 195 200 205

Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val
 210 215 220

Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys
 225 230 235 240

Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His
 245 250 255

Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Leu Ala
 260 265 270

Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Cys His Arg Ala
 275 280 285

Gln Glu Val Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu
 290 295 300

Leu Ser Cys Leu Pro Asn Trp Gly Glu Arg Ile Met Phe Leu Leu Ala
 305 310 315 320

Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His
 325 330 335

Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Gly Asn Asp Trp Phe
 340 345 350

Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met
 355 360 365

Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe
 370 375 380

Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg
 385 390 395 400

Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr
 405 410 415

Lys Ala Asn Val Phe Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu
 420 425 430

Ala Arg Asp Leu Ser Asn Pro Leu Pro Lys Asn Met Val Trp Glu Ala
 435 440 445

Leu Lys Thr Leu Gly
 450

<210> 73
 <211> 1362
 <212> DNA
 <213> *Primula vialii*

<220>
 <221> CDS
 <222> (1)..(1362)
 <223> Delta-6-Desaturase

<400> 73
 atg gct aac aaa tct cca cca aac ccc aaa aca ggt tac att acc agc 48
 Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser
 1 5 10 15
 tca gac ctg aaa ggg cac aac aaa gca gga gac cta tgg ata tca atc 96
 Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile
 20 25 30
 cac ggg gag gta tac gac gtg tcc tcg tgg gcc ggc ctt cac ccg ggg 144
 His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly
 35 40 45
 ggc agt gcc ccc ctc atg gcc ctc gca gga cac gac gta acc gac gct 192
 Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala
 50 55 60
 ttt cta gcg tat cat cct cct tct acc gcc cgc ctc ctc cct ccc ctc 240
 Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu
 65 70 75 80
 tcc acc aac ctc ctc ctt caa aac cac tcc gtc tcc ccc acc tcc tct 288
 Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser
 85 90 95
 gac tac cgc aaa ctc ctc cac aac ttc cat aaa att ggt atg ttc cgc 336
 Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg
 100 105 110
 gcc agg ggc cac act gct tac gcc acc ttc gtc atc atg ata gtg atg 384
 Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met

115	120	125	
ttt cta acg agc gtg acc gga gtc ctt tgc agc gac agt gcg tgg gtc Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val 130 135 140			432
cat ctg gct agc ggc gca gca atg ggg ttc gcc tgg atc cag tgc gga His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly 145 150 155 160			480
tgg ata ggt cac gac tct ggg cat tac cgg att atg tct gac agg aaa Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys 165 170 175			528
tgg aac tgg ttc gcg cag gtc ctg agc aca aac tgc ctc cag ggg atc Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile 180 185 190			576
agt atc ggg tgg tgg aag tgg aac cat aac gcc cac cac att gct tgc Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys 195 200 205			624
aat agc ctg gac tac gac ccc gac ctc cag tat atc cct ttg ctc gtg Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val 210 215 220			672
gtc tcc ccc aag ttc ttc aac tcc ctt act tct cgt ttc tac gac aag Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys 225 230 235 240			720
aag ctg aat ttc gac ggc gtg tca agg ttt ctg gtt tgc tac cag cac Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His 245 250 255			768
tgg acg ttt tat cca gtc atg tgt gtc gct agg cta aac atg atc gca Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala 260 265 270			816
cag tcg ttt ata acg ctt ttc tcg agc agg gag gtg ggt cat agg gcg Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala 275 280 285			864
caa gag att ttc gga ctt gct gtg ttt tgg gtt tgg ttt ccg ctc ctg Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu 290 295 300			912
ctc tct tgc tta cct aat tgg agc gag agg att atg ttt ctg cta gcg Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala 305 310 315 320			960
agc tat tcc gtt acg ggg ata cag cac gtg cag ttc agc ttg aac cat Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His 325 330 335			1008
ttt tct tcg gac gtc tac gtg ggc ccg cca gta gct aac gac tgg ttc Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe 340 345 350			1056
aag aaa cag act gct ggg aca ctt aac ata tcg tgc ccg gcg tgg atg Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met 355 360 365			1104
gac tgg ttc cat ggc ggg ttg cag ttt cag gtc gag cac cac ttg ttt Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe 370 375 380			1152
ccg cgg atg cct agg ggt cag ttt agg aag att tct cct ttt gtg agg Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg			1200

119

385	390	395	400	
gat ttg tgt aag aaa cac aac ttg cct tac aat atc gcg tct ttt act				1248
Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr				
	405	410	415	
aaa gca aac gtg ttg acg ctt aag acg ctg aga aat acg gcc att gag				1296
Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu				
	420	425	430	
gct cgg gac ctc tct aat ccg acc cca aag aat atg gtg tgg gaa gcc				1344
Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala				
	435	440	445	
gtc cac aca cac ggc tag				1362
Val His Thr His Gly				
	450			
<210> 74				
<211> 453				
<212> PRT				
<213> Primula vialii				
<400> 74				
Met Ala Asn Lys Ser Pro Pro Asn Pro Lys Thr Gly Tyr Ile Thr Ser				
1	5	10	15	
Ser Asp Leu Lys Gly His Asn Lys Ala Gly Asp Leu Trp Ile Ser Ile				
	20	25	30	
His Gly Glu Val Tyr Asp Val Ser Ser Trp Ala Gly Leu His Pro Gly				
	35	40	45	
Gly Ser Ala Pro Leu Met Ala Leu Ala Gly His Asp Val Thr Asp Ala				
	50	55	60	
Phe Leu Ala Tyr His Pro Pro Ser Thr Ala Arg Leu Leu Pro Pro Leu				
65	70	75	80	
Ser Thr Asn Leu Leu Leu Gln Asn His Ser Val Ser Pro Thr Ser Ser				
	85	90	95	
Asp Tyr Arg Lys Leu Leu His Asn Phe His Lys Ile Gly Met Phe Arg				
	100	105	110	
Ala Arg Gly His Thr Ala Tyr Ala Thr Phe Val Ile Met Ile Val Met				
	115	120	125	
Phe Leu Thr Ser Val Thr Gly Val Leu Cys Ser Asp Ser Ala Trp Val				
	130	135	140	
His Leu Ala Ser Gly Ala Ala Met Gly Phe Ala Trp Ile Gln Cys Gly				
145	150	155	160	
Trp Ile Gly His Asp Ser Gly His Tyr Arg Ile Met Ser Asp Arg Lys				
	165	170	175	

Trp Asn Trp Phe Ala Gln Val Leu Ser Thr Asn Cys Leu Gln Gly Ile
180 185 190

Ser Ile Gly Trp Trp Lys Trp Asn His Asn Ala His His Ile Ala Cys
195 200 205

Asn Ser Leu Asp Tyr Asp Pro Asp Leu Gln Tyr Ile Pro Leu Leu Val
210 215 220

Val Ser Pro Lys Phe Phe Asn Ser Leu Thr Ser Arg Phe Tyr Asp Lys
225 230 235 240

Lys Leu Asn Phe Asp Gly Val Ser Arg Phe Leu Val Cys Tyr Gln His
245 250 255

Trp Thr Phe Tyr Pro Val Met Cys Val Ala Arg Leu Asn Met Ile Ala
260 265 270

Gln Ser Phe Ile Thr Leu Phe Ser Ser Arg Glu Val Gly His Arg Ala
275 280 285

Gln Glu Ile Phe Gly Leu Ala Val Phe Trp Val Trp Phe Pro Leu Leu
290 295 300

Leu Ser Cys Leu Pro Asn Trp Ser Glu Arg Ile Met Phe Leu Leu Ala
305 310 315 320

Ser Tyr Ser Val Thr Gly Ile Gln His Val Gln Phe Ser Leu Asn His
325 330 335

Phe Ser Ser Asp Val Tyr Val Gly Pro Pro Val Ala Asn Asp Trp Phe
340 345 350

Lys Lys Gln Thr Ala Gly Thr Leu Asn Ile Ser Cys Pro Ala Trp Met
355 360 365

Asp Trp Phe His Gly Gly Leu Gln Phe Gln Val Glu His His Leu Phe
370 375 380

Pro Arg Met Pro Arg Gly Gln Phe Arg Lys Ile Ser Pro Phe Val Arg
385 390 395 400

Asp Leu Cys Lys Lys His Asn Leu Pro Tyr Asn Ile Ala Ser Phe Thr
405 410 415

Lys Ala Asn Val Leu Thr Leu Lys Thr Leu Arg Asn Thr Ala Ile Glu
420 425 430

Ala Arg Asp Leu Ser Asn Pro Thr Pro Lys Asn Met Val Trp Glu Ala
435 440 445

Val His Thr His Gly
450

<210> 75
<211> 903
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(903)
<223> Delta-5-Elongase

<400> 75
atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac 48
Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr
1 5 10 15
gcg tac gcg acg tac gcc tac gcc ttt gag tgg tgg cac gcg aat ggc 96
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
20 25 30
atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tgg ttg agg 144
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
35 40 45
ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
50 55 60
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65 70 75 80
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
85 90 95
atg ttc gcg cga gag atc tgg ggg ctg ggg cag ccc gtg tgg ggg tca 336
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
100 105 110
acc atg ccg tgg agc gat aga aaa tgg ttt aag atc ctc ctc ggg gtg 384
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
115 120 125
tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc 432
Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
130 135 140
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480
Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145 150 155 160
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528
His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
165 170 175
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tgg 576
Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180 185 190
ttc att cac atc gtg atg tac tgg tat tat ctc atg tgg gcg ctc ggc 624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly

122

195	200	205	
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln 210 215 220			672
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His 225 230 235 240			720
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met 245 250 255			768
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser 260 265 270			816
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala 275 280 285			864
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp 290 295 300			903

<210> 76

<211> 300

<212> PRT

<213> Ostreococcus tauri

<400> 76

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr
1 5 10 15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
20 25 30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
35 40 45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
50 55 60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65 70 75 80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
85 90 95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
115 120 125

Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
 145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
 165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
 180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
 195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
 210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
 225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
 245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
 260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
 290 295 300

<210> 77
 <211> 903
 <212> DNA
 <213> *Ostreococcus tauri*

<220>
 <221> CDS
 <222> (1)..(903)
 <223> Delta-5-Elongase

<400> 77
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
 1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
 20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
 35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly

124

50	55	60	
ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met 65 70 75 80			240
ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly 85 90 95			288
atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser 100 105 110			336
acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val 115 120 125			384
tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe 130 135 140			432
atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr 145 150 155 160			480
cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met 165 170 175			528
gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser 180 185 190			576
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly 195 200 205			624
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln 210 215 220			672
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His 225 230 235 240			720
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met 245 250 255			768
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser 260 265 270			816
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala 275 280 285			864
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp 290 295 300			903

<210> 78

<211> 300

<212> PRT

<213> *Ostreococcus tauri*

125

<400> 78

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
1 5 10 15

Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
20 25 30

Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
35 40 45

Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
50 55 60

Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
65 70 75 80

Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
85 90 95

Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
100 105 110

Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
115 120 125

Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
 275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
 290 295 300

<210> 79
 <211> 903
 <212> DNA
 <213> *Ostreococcus tauri*

<220>
 <221> CDS
 <222> (1)..(903)
 <223> Delta-5-Elongase

<400> 79
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg tcc gcc gcg tac 48
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr
 1 5 10 15
 gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
 20 25 30
 atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
 35 40 45
 ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
 50 55 60
 ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
 65 70 75 80
 ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
 85 90 95
 atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca 336
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
 100 105 110
 acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg 384
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
 115 120 125
 tgg ttg cac tac aac aac caa tat ttg gag cta ttg gac act gtg ttc 432
 Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe
 130 135 140
 atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
 145 150 155 160
 cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
 165 170 175
 gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg 576
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser

127

180	185	190	
ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc			624
Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly			
195	200	205	
att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa			672
Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln			
210	215	220	
ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac			720
Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His			
225	230	235	240
tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg			768
Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met			
	245	250	255
ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg			816
Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser			
	260	265	270
cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg			864
Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala			
	275	280	285
ccc agc gtg cga cgc acg cga tct cga aaa att gac taa			903
Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp			
290	295	300	

<210> 80
 <211> 300
 <212> PRT
 <213> *Ostreococcus tauri*

<400> 80

Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Ser Ala Ala Tyr			
1	5	10	15
Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly			
	20	25	30
Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg			
	35	40	45
Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly			
	50	55	60
Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met			
	65	70	75
Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly			
	85	90	95
Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser			
	100	105	110
Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val			
	115	120	125

Trp Leu His Tyr Asn Asn Gln Tyr Leu Glu Leu Leu Asp Thr Val Phe
130 135 140

Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
145 150 155 160

His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
165 170 175

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
290 295 300

<210> 81
<211> 879
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(879)
<223> Delta-6-Elongase

<400> 81
atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
1 5 10 15

tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
20 25 30

cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala

35	40	45	
att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val 50 55 60			192
aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys 65 70 75 80			240
att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala 85 90 95			288
ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln 100 105 110			336
gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr 115 120 125			384
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile 130 135 140			432
tac gag ttt gta gat act tac att atg ctt ctc aag aat aac ttg cgg Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg 145 150 155 160			480
caa gta aga ttc cta cac act tat cac cac agc acg att tcc ttt att Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile 165 170 175			528
tgg tgg atc att gct cgg agg gct ccg ggt ggt gat gct tac ttc agc Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser 180 185 190			576
gcg gcc ttg aac tca tgg gta cac gtg tgc atg tac acc tat tat cta Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu 195 200 205			624
tta tca acc ctt att gga aaa gaa gat cct aag cgt tcc aac tac ctt Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu 210 215 220			672
tgg tgg ggt cgc cac cta acg caa atg cag atg ctt cag ttt ttc ttc Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe 225 230 235 240			720
aac gta ctt caa gcg ttg tac tgc gct tcg ttc tct acg tat ccc aag Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys 245 250 255			768
ttt ttg tcc aaa att ctg ctc gtc tat atg atg agc ctt ctc ggc ttg Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu 260 265 270			816
ttt ggg cat ttc tac tat tcc aag cac ata gca gca gct aag ctc cag Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Lys Leu Gln 275 280 285			864
aaa aaa cag cag tga Lys Lys Gln Gln 290			879

<211> 292
 <212> PRT
 <213> *Ostreococcus tauri*

<400> 82

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
 1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
 20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
 35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
 50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
 65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
 85 90 95

Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
 100 105 110

Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
 115 120 125

Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
 130 135 140

Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
 145 150 155 160

Gln Val Arg Phe Leu His Thr Tyr His His Ser Thr Ile Ser Phe Ile
 165 170 175

Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
 180 185 190

Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
 195 200 205

Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu
 210 215 220

Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
 225 230 235 240

Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
 245 250 255

Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
 260 265 270

Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
 275 280 285

Lys Lys Gln Gln
 290

<210> 83
 <211> 831
 <212> DNA
 <213> Thraustochytrium sp.

<220>
 <221> CDS
 <222> (1)..(831)
 <223> Delta-5-Elongase

<400> 83
 atg gac gtc gtc gag cag caa tgg cgc cgc ttc gtg gac gcc gtg gac 48
 Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp
 1 5 10 15
 aac gga atc gtg gag ttc atg gag cat gag aag ccc aac aag ctg aac 96
 Asn Gly Ile Val Glu Phe Met Glu His Glu Lys Pro Asn Lys Leu Asn
 20 25 30
 gag ggc aag ctc ttc acc tcg acc gag gag atg atg gcg ctt atc gtc 144
 Glu Gly Lys Leu Phe Thr Ser Thr Glu Glu Met Met Ala Leu Ile Val
 35 40 45
 ggc tac ctg gcg ttc gtg gtc ctc ggg tcc gcc ttc atg aag gcc ttt 192
 Gly Tyr Leu Ala Phe Val Val Leu Gly Ser Ala Phe Met Lys Ala Phe
 50 55 60
 gtc gat aag cct ttc gag ctc aag ttc ctc aag ctc gtg cac aac atc 240
 Val Asp Lys Pro Phe Glu Leu Lys Phe Leu Lys Leu Val His Asn Ile
 65 70 75 80
 ttc ctc acc ggt ctg tcc atg tac atg gcc acc gag tgc gcg cgc cag 288
 Phe Leu Thr Gly Leu Ser Met Tyr Met Ala Thr Glu Cys Ala Arg Gln
 85 90 95
 gca tac ctc ggc ggc tac aag ctc ttt ggc aac ccg atg gag aag ggc 336
 Ala Tyr Leu Gly Gly Tyr Lys Leu Phe Gly Asn Pro Met Glu Lys Gly
 100 105 110
 acc gag tcg cac gcc ccg ggc atg gcc aac atc atc tac atc ttc tac 384
 Thr Glu Ser His Ala Pro Gly Met Ala Asn Ile Ile Tyr Ile Phe Tyr
 115 120 125
 gtg agc aag ttc ctc gaa ttc ctc gac acc gtc ttc atg atc ctc ggc 432
 Val Ser Lys Phe Leu Glu Phe Leu Asp Thr Val Phe Met Ile Leu Gly
 130 135 140
 aag aag tgg aag cag ctc agc ttt ctc cac gtc tac cac cac gcg agc 480
 Lys Lys Trp Lys Gln Leu Ser Phe Leu His Val Tyr His His Ala Ser
 145 150 155 160
 atc agc ttc atc tgg ggc atc atc gcc cgc ttc gcg ccc ggt ggc gac 528
 Ile Ser Phe Ile Trp Gly Ile Ile Ala Arg Phe Ala Pro Gly Gly Asp

132

165										170					175					
gcc	tac	ttc	tct	acc	atc	ctc	aac	agc	agc	gtg	cat	gtc	gtg	ctc	tac	576				
Ala	Tyr	Phe	Ser	Thr	Ile	Leu	Asn	Ser	Ser	Val	His	Val	Val	Leu	Tyr					
			180					185					190							
ggc	tac	tac	gcc	tcg	acc	acc	ctc	ggc	tac	acc	ttc	atg	cgc	ccg	ctg	624				
Gly	Tyr	Tyr	Ala	Ser	Thr	Thr	Leu	Gly	Tyr	Thr	Phe	Met	Arg	Pro	Leu					
			195				200					205								
cgc	ccg	tac	att	acc	acc	att	cag	ctc	acg	cag	ttc	atg	gcc	atg	gtc	672				
Arg	Pro	Tyr	Ile	Thr	Thr	Ile	Gln	Leu	Thr	Gln	Phe	Met	Ala	Met	Val					
	210					215					220									
gtc	cag	tcc	gtc	tat	gac	tac	tac	aac	ccc	tgc	gac	tac	ccg	cag	ccc	720				
Val	Gln	Ser	Val	Tyr	Asp	Tyr	Tyr	Asn	Pro	Cys	Asp	Tyr	Pro	Gln	Pro					
225					230					235					240					
ctc	gtc	aag	ctg	ctc	ttc	tgg	tac	atg	ctc	acc	atg	ctc	ggc	ctc	ttc	768				
Leu	Val	Lys	Leu	Leu	Phe	Trp	Tyr	Met	Leu	Thr	Met	Leu	Gly	Leu	Phe					
				245				250						255						
ggc	aac	ttc	ttc	gtg	cag	cag	tac	ctc	aag	ccc	aag	gcg	ccc	aag	aag	816				
Gly	Asn	Phe	Phe	Val	Gln	Gln	Tyr	Leu	Lys	Pro	Lys	Ala	Pro	Lys	Lys					
			260				265						270							
cag	aag	acc	atc	taa												831				
Gln	Lys	Thr	Ile																	
			275																	

<210> 84
 <211> 276
 <212> PRT
 <213> Thraustochytrium sp.

<400> 84

Met Asp Val Val Glu Gln Gln Trp Arg Arg Phe Val Asp Ala Val Asp
1 5 10 15

Asn Gly Ile Val Glu Phe Met Glu His Glu Lys Pro Asn Lys Leu Asn
20 25 30

Glu Gly Lys Leu Phe Thr Ser Thr Glu Glu Met Met Ala Leu Ile Val
35 40 45

Gly Tyr Leu Ala Phe Val Val Leu Gly Ser Ala Phe Met Lys Ala Phe
50 55 60

Val Asp Lys Pro Phe Glu Leu Lys Phe Leu Lys Leu Val His Asn Ile
65 70 75 80

Phe Leu Thr Gly Leu Ser Met Tyr Met Ala Thr Glu Cys Ala Arg Gln
85 90 95

Ala Tyr Leu Gly Gly Tyr Lys Leu Phe Gly Asn Pro Met Glu Lys Gly
100 105 110

Thr Glu Ser His Ala Pro Gly Met Ala Asn Ile Ile Tyr Ile Phe Tyr
115 120 125

Val Ser Lys Phe Leu Glu Phe Leu Asp Thr Val Phe Met Ile Leu Gly
 130 135 140

Lys Lys Trp Lys Gln Leu Ser Phe Leu His Val Tyr His His Ala Ser
 145 150 155 160

Ile Ser Phe Ile Trp Gly Ile Ile Ala Arg Phe Ala Pro Gly Gly Asp
 165 170 175

Ala Tyr Phe Ser Thr Ile Leu Asn Ser Ser Val His Val Val Leu Tyr
 180 185 190

Gly Tyr Tyr Ala Ser Thr Thr Leu Gly Tyr Thr Phe Met Arg Pro Leu
 195 200 205

Arg Pro Tyr Ile Thr Thr Ile Gln Leu Thr Gln Phe Met Ala Met Val
 210 215 220

Val Gln Ser Val Tyr Asp Tyr Tyr Asn Pro Cys Asp Tyr Pro Gln Pro
 225 230 235 240

Leu Val Lys Leu Leu Phe Trp Tyr Met Leu Thr Met Leu Gly Leu Phe
 245 250 255

Gly Asn Phe Phe Val Gln Gln Tyr Leu Lys Pro Lys Ala Pro Lys Lys
 260 265 270

Gln Lys Thr Ile
 275

<210> 85
 <211> 1077
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(1077)
 <223> Delta-5-Elongase

<400> 85
 atg tgc tca cca ccg ccg tca caa tcc aaa aca aca tcc ctc cta gca 48
 Met Cys Ser Pro Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala
 1 5 10 15

cgg tac acc acc gcc gcc ctc ctc ctc ctc acc ctc aca acg tgg tgc 96
 Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys
 20 25 30

cac ttc gcc ttc cca gcc gcc acc gcc aca ccc ggc ctc acc gcc gaa 144
 His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu
 35 40 45

atg cac tcc tac aaa gtc cca ctc ggt ctc acc gta ttc tac ctg ctg 192
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu

50	55	60	
agt cta ccg tca cta aag tac gtt acg gac aac tac ctt gcc aaa aag Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys 65 70 75 80			240
tat gat atg aag tca ctc ctg acg gaa tca atg gtg ttg tac aat gtg Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val 85 90 95			288
gcg caa gtg ctg ctc aat ggg tgg acg gtg tat gcg att gtg gat gcg Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala 100 105 110			336
gtg atg aat aga gac cat cct ttt att gga agt aga agt ttg gtt ggg Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly 115 120 125			384
gcg gcg ttg cat agt ggg agc tcg tat gcg gtg tgg gtt cat tat tgt Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys 130 135 140			432
gat aag tat ttg gag ttc ttt gat acg tat ttt atg gtg ttg agg ggg Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly 145 150 155 160			480
aaa atg gac cag gtc tcc ttc ctc cac atc tac cac cac acg acc ata Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile 165 170 175			528
gcg tgg gca tgg tgg atc gcc ctc cgc ttc tcc ccc ggc gga gac att Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile 180 185 190			576
tac ttc ggg gca ctc ctc aac tcc atc atc cac gtc ctc atg tat tcc Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser 195 200 205			624
tac tac gcc ctt gcc cta ctc aag gtc agt tgt cca tgg aaa cga tac Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr 210 215 220			672
ttg act caa gct caa tta ttg caa ttc aca agt gtg gtg gtt tat acg Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr 225 230 235 240			720
ggg tgt acg ggt tat act cat tac tat cat acg aag cat gga gcg gat Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp 245 250 255			768
gag aca cag cct agt tta gga acg tat tat ttc tgt tgt gga gtg cag Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln 260 265 270			816
gtg ttt gag atg gtt agt ttg ttt gta ctc ttt tcc atc ttt tat aaa Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys 275 280 285			864
cga tcc tat tcg aag aag aac aag tca gga gga aag gat agc aag aag Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys 290 295 300			912
aat gat gat ggg aat aat gag gat caa tgt cac aag gct atg aag gat Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp 305 310 315 320			960
ata tcg gag ggt gcg aag gag gtt gtg ggg cat gca gcg aag gat gct Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala 1008			

135

325 330 335
 gga aag ttg gtg gct acg gcg agt aag gct gta aag agg aag gga act 1056
 Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr
 340 345 350
 cgt gtt act ggt gcc atg tag 1077
 Arg Val Thr Gly Ala Met
 355
 <210> 86
 <211> 358
 <212> PRT
 <213> *Thalassiosira pseudonana*
 <400> 86
 Met Cys Ser Pro Pro Pro Ser Gln Ser Lys Thr Thr Ser Leu Leu Ala
 1 5 10 15
 Arg Tyr Thr Thr Ala Ala Leu Leu Leu Leu Thr Leu Thr Thr Trp Cys
 20 25 30
 His Phe Ala Phe Pro Ala Ala Thr Ala Thr Pro Gly Leu Thr Ala Glu
 35 40 45
 Met His Ser Tyr Lys Val Pro Leu Gly Leu Thr Val Phe Tyr Leu Leu
 50 55 60
 Ser Leu Pro Ser Leu Lys Tyr Val Thr Asp Asn Tyr Leu Ala Lys Lys
 65 70 75 80
 Tyr Asp Met Lys Ser Leu Leu Thr Glu Ser Met Val Leu Tyr Asn Val
 85 90 95
 Ala Gln Val Leu Leu Asn Gly Trp Thr Val Tyr Ala Ile Val Asp Ala
 100 105 110
 Val Met Asn Arg Asp His Pro Phe Ile Gly Ser Arg Ser Leu Val Gly
 115 120 125
 Ala Ala Leu His Ser Gly Ser Ser Tyr Ala Val Trp Val His Tyr Cys
 130 135 140
 Asp Lys Tyr Leu Glu Phe Phe Asp Thr Tyr Phe Met Val Leu Arg Gly
 145 150 155 160
 Lys Met Asp Gln Val Ser Phe Leu His Ile Tyr His His Thr Thr Ile
 165 170 175
 Ala Trp Ala Trp Trp Ile Ala Leu Arg Phe Ser Pro Gly Gly Asp Ile
 180 185 190
 Tyr Phe Gly Ala Leu Leu Asn Ser Ile Ile His Val Leu Met Tyr Ser
 195 200 205

Tyr Tyr Ala Leu Ala Leu Leu Lys Val Ser Cys Pro Trp Lys Arg Tyr
 210 215 220

Leu Thr Gln Ala Gln Leu Leu Gln Phe Thr Ser Val Val Val Tyr Thr
 225 230 235 240

Gly Cys Thr Gly Tyr Thr His Tyr Tyr His Thr Lys His Gly Ala Asp
 245 250 255

Glu Thr Gln Pro Ser Leu Gly Thr Tyr Tyr Phe Cys Cys Gly Val Gln
 260 265 270

Val Phe Glu Met Val Ser Leu Phe Val Leu Phe Ser Ile Phe Tyr Lys
 275 280 285

Arg Ser Tyr Ser Lys Lys Asn Lys Ser Gly Gly Lys Asp Ser Lys Lys
 290 295 300

Asn Asp Asp Gly Asn Asn Glu Asp Gln Cys His Lys Ala Met Lys Asp
 305 310 315 320

Ile Ser Glu Gly Ala Lys Glu Val Val Gly His Ala Ala Lys Asp Ala
 325 330 335

Gly Lys Leu Val Ala Thr Ala Ser Lys Ala Val Lys Arg Lys Gly Thr
 340 345 350

Arg Val Thr Gly Ala Met
 355

<210> 87
 <211> 1086
 <212> DNA
 <213> Phytophthora infestans

<220>
 <221> CDS
 <222> (1)..(1086)
 <223> Omega-3-Desaturase

<400> 87
 atg gcg acg aag gag gcg tat gtg ttc ccc act ctg acg gag atc aag 48
 Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
 1 5 10 15

cgg tcg cta cct aaa gac tgt ttc gag gct tcg gtg cct ctg tcg ctc 96
 Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
 20 25 30

tac tac acc gtg cgt tgt ctg gtg atc gcg gtg gct cta acc ttc ggt 144
 Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
 35 40 45

ctc aac tac gct cgc gct ctg ccc gag gtc gag agc ttc tgg gct ctg 192
 Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu

137

50	55	60	
gac gcc gca ctc tgc acg ggc tac atc ttg ctg cag ggc atc gtg ttc Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe 65 70 75 80			240
tgg ggc ttc ttc acg gtg ggc cac gat gcc ggc cac ggc gcc ttc tcg Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser 85 90 95			288
cgc tac cac ctg ctt aac ttc gtg gtg ggc act ttc atg cac tcg ctc Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu 100 105 110			336
atc ctc acg ccc ttc gag tcg tgg aag ctc acg cac cgt cac cac cac Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His 115 120 125			384
aag aac acg ggc aac att gac cgt gac gag gtc ttc tac ccg caa cgc Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg 130 135 140			432
aag gcc gac gac cac ccg ctg tct cgc aac ctg att ctg gcg ctc ggg Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly 145 150 155 160			480
gca gcg tgg ctc gcc tat ttg gtc gag ggc ttc cct cct cgt aag gtc Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val 165 170 175			528
aac cac ttc aac ccg ttc gag cct ctg ttc gtg cgt cag gtg tca gct Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala 180 185 190			576
gtg gta atc tct ctt ctc gcc cac ttc ttc gtg gcc gga ctc tcc atc Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile 195 200 205			624
tat ctg agc ctc cag ctg ggc ctt aag acg atg gca atc tac tac tat Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr 210 215 220			672
gga cct gtt ttt gtg ttc ggc agc atg ctg gtc att acc acc ttc cta Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu 225 230 235 240			720
cac cac aat gat gag gag acc cca tgg tac gcc gac tcg gag tgg acg His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr 245 250 255			768
tac gtc aag ggc aac ctc tcg tcc gtg gac cga tcg tac ggc gcg ctc Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu 260 265 270			816
att gac aac ctg agc cac aac atc ggc acg cac cag atc cac cac ctt Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu 275 280 285			864
ttc cct atc att ccg cac tac aaa ctc aag aaa gcc act gcg gcc ttc Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe 290 295 300			912
cac cag gct ttc cct gag ctc gtg cgc aag agc gac gag cca att atc His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile 305 310 315 320			960
aag gct ttc ttc cgg gtt gga cgt ctc tac gca aac tac ggc gtt gtg Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val 325 330 335 340			1008

138

325 330 335 1056
gac cag gag gcg aag ctc ttc acg cta aag gaa gcc aag gcg gcg acc
Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr
340 345 350

gag gcg gcg gcc aag acc aag tcc acg taa 1086
Glu Ala Ala Ala Lys Thr Lys Ser Thr
355 360

<210> 88
<211> 361
<212> PRT
<213> Phytophthora infestans

<400> 88

Met Ala Thr Lys Glu Ala Tyr Val Phe Pro Thr Leu Thr Glu Ile Lys
1 5 10 15

Arg Ser Leu Pro Lys Asp Cys Phe Glu Ala Ser Val Pro Leu Ser Leu
20 25 30

Tyr Tyr Thr Val Arg Cys Leu Val Ile Ala Val Ala Leu Thr Phe Gly
35 40 45

Leu Asn Tyr Ala Arg Ala Leu Pro Glu Val Glu Ser Phe Trp Ala Leu
50 55 60

Asp Ala Ala Leu Cys Thr Gly Tyr Ile Leu Leu Gln Gly Ile Val Phe
65 70 75 80

Trp Gly Phe Phe Thr Val Gly His Asp Ala Gly His Gly Ala Phe Ser
85 90 95

Arg Tyr His Leu Leu Asn Phe Val Val Gly Thr Phe Met His Ser Leu
100 105 110

Ile Leu Thr Pro Phe Glu Ser Trp Lys Leu Thr His Arg His His His
115 120 125

Lys Asn Thr Gly Asn Ile Asp Arg Asp Glu Val Phe Tyr Pro Gln Arg
130 135 140

Lys Ala Asp Asp His Pro Leu Ser Arg Asn Leu Ile Leu Ala Leu Gly
145 150 155 160

Ala Ala Trp Leu Ala Tyr Leu Val Glu Gly Phe Pro Pro Arg Lys Val
165 170 175

Asn His Phe Asn Pro Phe Glu Pro Leu Phe Val Arg Gln Val Ser Ala
180 185 190

Val Val Ile Ser Leu Leu Ala His Phe Phe Val Ala Gly Leu Ser Ile
195 200 205

Tyr Leu Ser Leu Gln Leu Gly Leu Lys Thr Met Ala Ile Tyr Tyr Tyr
210 215 220

Gly Pro Val Phe Val Phe Gly Ser Met Leu Val Ile Thr Thr Phe Leu
225 230 235 240

His His Asn Asp Glu Glu Thr Pro Trp Tyr Ala Asp Ser Glu Trp Thr
245 250 255

Tyr Val Lys Gly Asn Leu Ser Ser Val Asp Arg Ser Tyr Gly Ala Leu
260 265 270

Ile Asp Asn Leu Ser His Asn Ile Gly Thr His Gln Ile His His Leu
275 280 285

Phe Pro Ile Ile Pro His Tyr Lys Leu Lys Lys Ala Thr Ala Ala Phe
290 295 300

His Gln Ala Phe Pro Glu Leu Val Arg Lys Ser Asp Glu Pro Ile Ile
305 310 315 320

Lys Ala Phe Phe Arg Val Gly Arg Leu Tyr Ala Asn Tyr Gly Val Val
325 330 335

Asp Gln Glu Ala Lys Leu Phe Thr Leu Lys Glu Ala Lys Ala Ala Thr
340 345 350

Glu Ala Ala Ala Lys Thr Lys Ser Thr
355 360

<210> 89
<211> 1371
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(1371)
<223> Delta-6-Desaturase

<400> 89
atg tgc gtg gag acg gaa aat aac gat ggg atc ccc acg gtg gag atc 48
Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile
1 5 10 15
gcg ttc gac ggt gag cgc gag cgg gcg gag gca aac gtg aag ctg tcc 96
Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser
20 25 30
gcg gag aag atg gag ccg gcg gcg ctg gcg aag acg ttc gcg agg cgg 144
Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
35 40 45
tac gtc gtg atc gag ggg gtg gag tac gat gtg acg gat ttt aag cac 192
Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His

140

50	55	60	
ccg gga gga acg gtt att ttc tat gcg ttg tca aac acc ggg gcg gac Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp 65 70 75 80			240
gcg acg gaa gcg ttc aag gag ttt cat cat cgg tcg aga aag gcg agg Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg 85 90 95			288
aaa gcc ttg gcg gcg ctc ccg tct cga ccg gcc aag acg gcc aag gtg Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val 100 105 110			336
gac gac gcg gag atg ctc caa gat ttc gcc aag tgg cgg aaa gaa ttg Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu 115 120 125			384
gag aga gat gga ttc ttc aag ccc tct ccg gcg cac gtg gcg tat cgc Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg 130 135 140			432
ttc gcc gag ctc gcg gcg atg tac gct ctc ggg acg tac ctg atg tac Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr 145 150 155 160			480
gct cga tac gtc gtc tcc tcg gtg ctc gtg tac gct tgc ttt ttc ggc Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly 165 170 175			528
gcc cga tgc ggt tgg gtg cag cac gag ggc gga cac agc tcg ctg acg Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr 180 185 190			576
ggc aac att tgg tgg gac aag cgc atc cag gcc ttc aca gcc ggg ttc Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe 195 200 205			624
ggt ctc gcc ggt agc ggc gac atg tgg aac tcg atg cac aac aag cat Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His 210 215 220			672
cac gcg acg cct caa aag gtt cgt cac gac atg gat ctg gac acc acc His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr 225 230 235 240			720
ccc gcg gtg gcg ttc ttc aac acc gcg gtg gaa gac aat cgt ccc cgt Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg 245 250 255			768
ggc ttt agc aag tac tgg ttg cgc ctt cag gcg tgg acc ttc atc ccc Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro 260 265 270			816
gtg acg tcc ggc ttg gtg ctc ctt ttc tgg atg ttt ttc ctc cac ccc Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro 275 280 285			864
tcc aag gct ttg aag ggt ggc aag tac gaa gag ttg gtg tgg atg ctc Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu 290 295 300			912
gcc gcg cac gtc atc cgc acg tgg acg atc aag gcg gtg acc gga ttc Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe 305 310 315 320			960
acc gcg atg cag tcc tac ggc tta ttt ttg gcg acg agc tgg gtg agc Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser 1008			

141

325										330					335					
ggc tgc tat ctg ttt gca cac ttc tcc acg tcg cac acg cac ctg gat																	1056			
Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp																				
			340						345						350					
gtg gtg ccc gcg gac gag cat ctc tcc tgg gtt cga tac gcc gtc gat																	1104			
Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp																				
		355						360					365							
cac acg atc gac atc gat ccg agt caa ggt tgg gtg aac tgg ttg atg																	1152			
His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met																				
		370				375						380								
ggc tac ctc aac tgc caa gtc atc cac cac ctc ttt ccg agc atg ccg																	1200			
Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro																				
		385				390					395					400				
cag ttc cgc cag ccc gag gta tct cgc cgc ttc gtc gcc ttt gcg aaa																	1248			
Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys																				
			405						410							415				
aag tgg aac ctc aac tac aag gtc atg acc tac gcc ggt gcg tgg aag																	1296			
Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys																				
		420						425						430						
gca acg ctc gga aac ctc gac aac gtg ggt aag cac tac tac gtg cac																	1344			
Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His																				
		435					440						445							
ggc caa cac tcc gga aag acg gcg taa																	1371			
Gly Gln His Ser Gly Lys Thr Ala																				
		450					455													

<210> 90

<211> 456

<212> PRT

<213> Ostreococcus tauri

<400> 90

Met Cys Val Glu Thr Glu Asn Asn Asp Gly Ile Pro Thr Val Glu Ile																
1				5					10						15	

Ala Phe Asp Gly Glu Arg Glu Arg Ala Glu Ala Asn Val Lys Leu Ser																
			20					25						30		

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg																
		35					40					45				

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His																
	50					55					60					

Pro Gly Gly Thr Val Ile Phe Tyr Ala Leu Ser Asn Thr Gly Ala Asp																
65					70				75					80		

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg																
			85					90						95		

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val																
			100				105						110			

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu
 115 120 125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg
 130 135 140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr
 145 150 155 160

Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly
 165 170 175

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr
 180 185 190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
 195 200 205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
 210 215 220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
 225 230 235 240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
 245 250 255

Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro
 260 265 270

Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro
 275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu
 290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe
 305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser
 325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp
 340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp
 355 360 365

His Thr Ile Asp Ile Asp Pro Ser Gln Gly Trp Val Asn Trp Leu Met
 370 375 380

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro
385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys
405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys
420 425 430

Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His
435 440 445

Gly Gln His Ser Gly Lys Thr Ala
450 455

<210> 91
<211> 606
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(606)
<223> Delta-5-Desaturase

<400> 91
atg tac ggt ttg cta tcg ctc aag tcg tgc ttc gtc gac gat ttc aac 48
Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn
1 5 10 15
gcc tac ttc tcc gga cgc atc ggc tgg gtc aag gtg atg aag ttc acc 96
Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys Phe Thr
20 25 30
cgc ggc gag gcg atc gca ttt tgg ggc acc aag ctc ttg tgg gcc gcg 144
Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp Ala Ala
35 40 45
tat tac ctc gcg ttg ccg cta aag atg tcg cat cgg ccg ctc gga gaa 192
Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu Gly Glu
50 55 60
ctc ctc gca ctc tgg gcc gtc acc gag ttc gtc acc gga tgg ctg ttg 240
Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp Leu Leu
65 70 75 80
gcg ttc atg ttc caa gtc gcc cac gtc gtc ggc gag gtt cac ttc ttc 288
Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His Phe Phe
85 90 95
acc ctc gac gcg aag aac cgc gtg aac ttg gga tgg gga gag gca cag 336
Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu Ala Gln
100 105 110
ctc atg tcg agc gcg gat ttc gcc cac gga tcc aag ttt tgg acg cac 384
Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp Thr His
115 120 125
ttc tcc gga ggc tta aac tac caa gtc gtc cac cat ctc ttc ccg ggc 432
Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe Pro Gly

144

130	135	140	
gtc tgc cac gtg cac tat ccc gcg ctc gcg cca att att aag gcg gca			480
Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys Ala Ala			
145	150	155	160
gct gag aag cac ggc ctc cac tac cag att tac ccc acg ttt tgg tcc			528
Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe Trp Ser			
	165	170	175
gcc ctg cgc gcg cac ttc cgg cac ctc gcc aac gtc ggc cgc gcc gcg			576
Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg Ala Ala			
	180	185	190
tac gta ccg tcc ctc caa acc gtc gga tga			606
Tyr Val Pro Ser Leu Gln Thr Val Gly			
	195	200	
<210> 92			
<211> 201			
<212> PRT			
<213> <i>Ostreococcus tauri</i>			
<400> 92			
Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp Phe Asn			
1	5	10	15
Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys Phe Thr			
	20	25	30
Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp Ala Ala			
	35	40	45
Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu Gly Glu			
	50	55	60
Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp Leu Leu			
	65	70	75
Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His Phe Phe			
	85	90	95
Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu Ala Gln			
	100	105	110
Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp Thr His			
	115	120	125
Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe Pro Gly			
	130	135	140
Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys Ala Ala			
	145	150	155
Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe Trp Ser			
	165	170	175

Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg Ala Ala
 180 185 190

Tyr Val Pro Ser Leu Gln Thr Val Gly
 195 200

<210> 93
 <211> 714
 <212> DNA
 <213> *Ostreococcus tauri*

<220>
 <221> CDS
 <222> (1)..(714)
 <223> Delta-5-Desaturase

<400> 93
 atg gtg agc cat cac tcg tac tgt aac gac gcg gat ttg gat cag gat 48
 Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp
 1 5 10 15
 gtg tac acc gca ctg ccg ctc ctg cgc ctg gac ccg tct cag gag ttg 96
 Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu
 20 25 30
 aag tgg ttt cat cga tac cag gcg ttt tac gcc ccg ctc atg tgg ccg 144
 Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro
 35 40 45
 ttt ttg tgg ctc gcg gcg cag ttt ggc gac gcg cag aac atc ctg atc 192
 Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile
 50 55 60
 gac cga gcg tcg ccg ggc gtc gcg tac aag gga ttg atg gcg aac gag 240
 Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu
 65 70 75 80
 gtc gcg ctg tac gtt ctc ggt aag gtt tta cac ttt ggt ctt ctc ctc 288
 Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu
 85 90 95
 ggc gtt cct gcg tac ttg cac gga ttg tcc aac gcg atc gtt cca ttc 336
 Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe
 100 105 110
 ttg gcg tac ggc gca ttc ggc tcc ttc gtc ctg tgc tgg ttc ttc atc 384
 Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile
 115 120 125
 gtc agc cat aac ctc gaa gcg ctg aca ccc gtt aac ctt aac aag tcc 432
 Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser
 130 135 140
 acg aag aac gac tgg ggg gcg tgg cag atc gag aca tcg gcg tct tgg 480
 Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp
 145 150 155 160
 ggc aac gcg ttc tgg agc ttc ttc tct gga ggt ctg aac ctg caa atc 528
 Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile
 165 170 175
 gag cac cac ctc ttc ccg ggc atg gcg cac aac ctg tac ccg aag atg 576
 Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met

146

180	185	190	
gtg ccg atc atc aag gac gag tgt gcg aaa gcg ggc gtt cgc tac acc			624
Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr			
195	200	205	
ggg tac ggt ggc tac acc ggc ctg ctc ccg atc acc cgc gac atg ttc			672
Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe			
210	215	220	
tcc tac ctc cat aag tgt ggc cga acg gcg aaa cta gcc taa			714
Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala			
225	230	235	

<210> 94
 <211> 237
 <212> PRT
 <213> *Ostreococcus tauri*

<400> 94

Met Val Ser His His Ser Tyr Cys Asn Asp Ala Asp Leu Asp Gln Asp			
1	5	10	15
Val Tyr Thr Ala Leu Pro Leu Leu Arg Leu Asp Pro Ser Gln Glu Leu			
	20	25	30
Lys Trp Phe His Arg Tyr Gln Ala Phe Tyr Ala Pro Leu Met Trp Pro			
	35	40	45
Phe Leu Trp Leu Ala Ala Gln Phe Gly Asp Ala Gln Asn Ile Leu Ile			
	50	55	60
Asp Arg Ala Ser Pro Gly Val Ala Tyr Lys Gly Leu Met Ala Asn Glu			
65	70	75	80
Val Ala Leu Tyr Val Leu Gly Lys Val Leu His Phe Gly Leu Leu Leu			
	85	90	95
Gly Val Pro Ala Tyr Leu His Gly Leu Ser Asn Ala Ile Val Pro Phe			
	100	105	110
Leu Ala Tyr Gly Ala Phe Gly Ser Phe Val Leu Cys Trp Phe Phe Ile			
	115	120	125
Val Ser His Asn Leu Glu Ala Leu Thr Pro Val Asn Leu Asn Lys Ser			
	130	135	140
Thr Lys Asn Asp Trp Gly Ala Trp Gln Ile Glu Thr Ser Ala Ser Trp			
145	150	155	160
Gly Asn Ala Phe Trp Ser Phe Phe Ser Gly Gly Leu Asn Leu Gln Ile			
	165	170	175
Glu His His Leu Phe Pro Gly Met Ala His Asn Leu Tyr Pro Lys Met			
	180	185	190

Val Pro Ile Ile Lys Asp Glu Cys Ala Lys Ala Gly Val Arg Tyr Thr
 195 200 205

Gly Tyr Gly Gly Tyr Thr Gly Leu Leu Pro Ile Thr Arg Asp Met Phe
 210 215 220

Ser Tyr Leu His Lys Cys Gly Arg Thr Ala Lys Leu Ala
 225 230 235

<210> 95
 <211> 1611
 <212> DNA
 <213> *Ostreococcus tauri*

<220>
 <221> CDS
 <222> (1)..(1611)
 <223> Delta-4-Desaturase

<400> 95
 atg tac ctc gga cgc ggc cgt ctc gag agc ggg acg acg cga ggg atg 48
 Met Tyr Leu Gly Arg Gly Arg Leu Glu Ser Gly Thr Thr Arg Gly Met
 1 5 10 15
 atg cgg acg cac gcg cgg cga ccg tcg acg acg tcg aat ccg tgc gcg 96
 Met Arg Thr His Ala Arg Arg Pro Ser Thr Thr Ser Asn Pro Cys Ala
 20 25 30
 cgg tca cgc gtg cgt aag acg acg gag cga tcg ctc gcg cga gtg cga 144
 Arg Ser Arg Val Arg Lys Thr Thr Glu Arg Ser Leu Ala Arg Val Arg
 35 40 45
 cga tcg acg agt gag aag gga agc gcg ctc gtg ctc gag cga gag agc 192
 Arg Ser Thr Ser Glu Lys Gly Ser Ala Leu Val Leu Glu Arg Glu Ser
 50 55 60
 gaa cgg gag aag gag gag gga ggg aaa gcg cga gcg gag gga ttg cga 240
 Glu Arg Glu Lys Glu Glu Gly Gly Lys Ala Arg Ala Glu Gly Leu Arg
 65 70 75 80
 ttc caa cgc ccg gac gtc gcc gcg ccg ggg gga gcg gat cct tgg aac 288
 Phe Gln Arg Pro Asp Val Ala Ala Pro Gly Gly Ala Asp Pro Trp Asn
 85 90 95
 gac gag aag tgg aca aag acc aag tgg acg gta ttc aga gac gtc gcg 336
 Asp Glu Lys Trp Thr Lys Thr Lys Trp Thr Val Phe Arg Asp Val Ala
 100 105 110
 tac gat ctc gat cct ttc ttc gct cga cac ccc gga gga gac tgg ctc 384
 Tyr Asp Leu Asp Pro Phe Phe Ala Arg His Pro Gly Gly Asp Trp Leu
 115 120 125
 ctg aac ttg gcc gtg gga cga gac tgc acc gcg ctc atc gaa tcc tat 432
 Leu Asn Leu Ala Val Gly Arg Asp Cys Thr Ala Leu Ile Glu Ser Tyr
 130 135 140
 cac ttg cga cca gag gtg gcg acg gct cgt ttc aga atg ctg ccc aaa 480
 His Leu Arg Pro Glu Val Ala Thr Ala Arg Phe Arg Met Leu Pro Lys
 145 150 155 160
 ctc gag gat ttt ccc gtc gag gcc gtg ccc aag tcc ccg aga ccg aac 528
 Leu Glu Asp Phe Pro Val Glu Ala Val Pro Lys Ser Pro Arg Pro Asn

148

165								170					175				
gat	tcg	ccg	tta	tac	aac	aac	att	cgc	aac	cga	gtc	cgc	gaa	gag	ctc	576	
Asp	Ser	Pro	Leu	Tyr	Asn	Asn	Ile	Arg	Asn	Arg	Val	Arg	Glu	Glu	Leu		
			180					185					190				
ttc	cca	gag	gag	gga	aag	aat	atg	cac	aga	cag	ggc	ggc	gac	cac	ggc	624	
Phe	Pro	Glu	Glu	Gly	Lys	Asn	Met	His	Arg	Gln	Gly	Gly	Asp	His	Gly		
			195				200					205					
gac	ggt	gac	gat	tct	ggg	ttt	cgc	cgc	ctt	ttg	ctt	atg	ccg	tgt	acc	672	
Asp	Gly	Asp	Asp	Ser	Gly	Phe	Arg	Arg	Leu	Leu	Leu	Met	Pro	Cys	Thr		
	210					215					220						
tat	tcc	ctt	ccg	ggg	gtt	cct	ttc	cgg	ctg	cct	cct	cgg	gtc	tcg	cgg	720	
Tyr	Ser	Leu	Pro	Gly	Val	Pro	Phe	Arg	Leu	Pro	Pro	Arg	Val	Ser	Arg		
					230					235					240		
ggg	cgt	gga	ttg	gtc	tca	cga	ttc	agg	cac	tgc	gcc	aac	cac	ggc	gcg	768	
Gly	Arg	Gly	Leu	Val	Ser	Arg	Phe	Arg	His	Cys	Ala	Asn	His	Gly	Ala		
				245					250					255			
atg	tct	cct	tcg	ccg	gcc	gtt	aac	ggc	gtc	ctc	ggg	ttg	acg	aac	gat	816	
Met	Ser	Pro	Ser	Pro	Ala	Val	Asn	Gly	Val	Leu	Gly	Leu	Thr	Asn	Asp		
			260					265					270				
ctc	atc	ggc	ggc	tcg	tcc	ttg	atg	tgg	aga	tat	cac	cac	caa	gtc	agc	864	
Leu	Ile	Gly	Gly	Ser	Ser	Leu	Met	Trp	Arg	Tyr	His	His	Gln	Val	Ser		
		275					280					285					
cac	cac	att	cat	tgc	aac	gac	aac	gcc	atg	gat	caa	gac	gtg	tac	acg	912	
His	His	Ile	His	Cys	Asn	Asp	Asn	Ala	Met	Asp	Gln	Asp	Val	Tyr	Thr		
		290				295					300						
gcg	atg	cca	tta	ttg	cgt	ttc	gac	gct	cgc	cgg	ccc	aag	tcc	tgg	tac	960	
Ala	Met	Pro	Leu	Leu	Arg	Phe	Asp	Ala	Arg	Arg	Pro	Lys	Ser	Trp	Tyr		
	305				310					315					320		
cat	cgc	ttc	cag	cag	tgg	tac	atg	ttt	tta	gcg	ttc	ccg	ttg	ttg	cag	1008	
His	Arg	Phe	Gln	Gln	Trp	Tyr	Met	Phe	Leu	Ala	Phe	Pro	Leu	Leu	Gln		
			325						330					335			
gtt	gcc	ttc	caa	gtc	gga	gac	att	gcc	gca	ctg	ttc	acg	cgt	gat	acc	1056	
Val	Ala	Phe	Gln	Val	Gly	Asp	Ile	Ala	Ala	Leu	Phe	Thr	Arg	Asp	Thr		
			340					345					350				
gaa	ggc	gct	aag	ctt	cac	ggg	gcg	acg	acg	tgg	gag	ctt	acc	acg	gtt	1104	
Glu	Gly	Ala	Lys	Leu	His	Gly	Ala	Thr	Thr	Trp	Glu	Leu	Thr	Thr	Val		
		355				360						365					
gtc	ctc	ggt	aag	att	gtg	cac	ttc	ggt	ctt	ttg	ttg	ggg	ccg	ttg	atg	1152	
Val	Leu	Gly	Lys	Ile	Val	His	Phe	Gly	Leu	Leu	Leu	Gly	Pro	Leu	Met		
		370				375						380					
aac	cac	gcg	gtg	agt	tct	gtt	ttg	ctg	ggg	atc	gtc	ggt	ttc	atg	gcg	1200	
Asn	His	Ala	Val	Ser	Ser	Val	Leu	Leu	Gly	Ile	Val	Gly	Phe	Met	Ala		
					390					395					400		
tgc	caa	ggt	ata	gtt	ctg	gcg	tgc	acg	ttt	gct	gtg	agt	cac	aat	gtc	1248	
Cys	Gln	Gly	Ile	Val	Leu	Ala	Cys	Thr	Phe	Ala	Val	Ser	His	Asn	Val		
			405						410					415			
gcg	gag	gcg	aag	ata	cct	gag	gac	acc	gga	gga	gaa	gcc	tgg	gag	aga	1296	
Ala	Glu	Ala	Lys	Ile	Pro	Glu	Asp	Thr	Gly	Gly	Glu	Ala	Trp	Glu	Arg		
			420					425					430				
gat	tgg	ggt	gtc	cag	cag	ttg	gtg	act	agc	gcc	gac	tgg	ggt	gga	aag	1344	
Asp	Trp	Gly	Val	Gln	Gln	Leu	Val	Thr	Ser	Ala	Asp	Trp	Gly	Gly	Lys		

149

435	440	445	
ata ggt aac ttc ttc acg ggt ggc ctc aac ttg caa gtt gag cac cac Ile Gly Asn Phe Phe Thr Gly Gly Leu Asn Leu Gln Val Glu His His 450 455 460			1392
ttg ttt ccg gcg att tgc ttc gtc cac tac ccg gac atc gcg aag atc Leu Phe Pro Ala Ile Cys Phe Val His Tyr Pro Asp Ile Ala Lys Ile 465 470 475 480			1440
gtg aag gaa gaa gcg gcc aag ctc aac atc cct tac gcg tct tac agg Val Lys Glu Glu Ala Ala Lys Leu Asn Ile Pro Tyr Ala Ser Tyr Arg 485 490 495			1488
act ctt cct ggt att ttc gtc caa ttc tgg aga ttt atg aag gac atg Thr Leu Pro Gly Ile Phe Val Gln Phe Trp Arg Phe Met Lys Asp Met 500 505 510			1536
ggc acg gct gag caa att ggt gaa gtt cca ttg ccg aag att ccc aac Gly Thr Ala Glu Gln Ile Gly Glu Val Pro Leu Pro Lys Ile Pro Asn 515 520 525			1584
ccg cag ctc gcg ccg aag ctc gct tag Pro Gln Leu Ala Pro Lys Leu Ala 530 535			1611

<210> 96

<211> 536

<212> PRT

<213> *Ostreococcus tauri*

<400> 96

Met Tyr Leu Gly Arg Gly Arg Leu Glu Ser Gly Thr Thr Arg Gly Met
1 5 10 15

Met Arg Thr His Ala Arg Arg Pro Ser Thr Thr Ser Asn Pro Cys Ala
20 25 30

Arg Ser Arg Val Arg Lys Thr Thr Glu Arg Ser Leu Ala Arg Val Arg
35 40 45

Arg Ser Thr Ser Glu Lys Gly Ser Ala Leu Val Leu Glu Arg Glu Ser
50 55 60

Glu Arg Glu Lys Glu Glu Gly Gly Lys Ala Arg Ala Glu Gly Leu Arg
65 70 75 80

Phe Gln Arg Pro Asp Val Ala Ala Pro Gly Gly Ala Asp Pro Trp Asn
85 90 95

Asp Glu Lys Trp Thr Lys Thr Lys Trp Thr Val Phe Arg Asp Val Ala
100 105 110

Tyr Asp Leu Asp Pro Phe Phe Ala Arg His Pro Gly Gly Asp Trp Leu
115 120 125

Leu Asn Leu Ala Val Gly Arg Asp Cys Thr Ala Leu Ile Glu Ser Tyr
130 135 140

His Leu Arg Pro Glu Val Ala Thr Ala Arg Phe Arg Met Leu Pro Lys
 145 150 155 160

Leu Glu Asp Phe Pro Val Glu Ala Val Pro Lys Ser Pro Arg Pro Asn
 165 170 175

Asp Ser Pro Leu Tyr Asn Asn Ile Arg Asn Arg Val Arg Glu Glu Leu
 180 185 190

Phe Pro Glu Glu Gly Lys Asn Met His Arg Gln Gly Gly Asp His Gly
 195 200 205

Asp Gly Asp Asp Ser Gly Phe Arg Arg Leu Leu Leu Met Pro Cys Thr
 210 215 220

Tyr Ser Leu Pro Gly Val Pro Phe Arg Leu Pro Pro Arg Val Ser Arg
 225 230 235 240

Gly Arg Gly Leu Val Ser Arg Phe Arg His Cys Ala Asn His Gly Ala
 245 250 255

Met Ser Pro Ser Pro Ala Val Asn Gly Val Leu Gly Leu Thr Asn Asp
 260 265 270

Leu Ile Gly Gly Ser Ser Leu Met Trp Arg Tyr His His Gln Val Ser
 275 280 285

His His Ile His Cys Asn Asp Asn Ala Met Asp Gln Asp Val Tyr Thr
 290 295 300

Ala Met Pro Leu Leu Arg Phe Asp Ala Arg Arg Pro Lys Ser Trp Tyr
 305 310 315 320

His Arg Phe Gln Gln Trp Tyr Met Phe Leu Ala Phe Pro Leu Leu Gln
 325 330 335

Val Ala Phe Gln Val Gly Asp Ile Ala Ala Leu Phe Thr Arg Asp Thr
 340 345 350

Glu Gly Ala Lys Leu His Gly Ala Thr Thr Trp Glu Leu Thr Thr Val
 355 360 365

Val Leu Gly Lys Ile Val His Phe Gly Leu Leu Leu Gly Pro Leu Met
 370 375 380

Asn His Ala Val Ser Ser Val Leu Leu Gly Ile Val Gly Phe Met Ala
 385 390 395 400

Cys Gln Gly Ile Val Leu Ala Cys Thr Phe Ala Val Ser His Asn Val
 405 410 415

Ala Glu Ala Lys Ile Pro Glu Asp Thr Gly Gly Glu Ala Trp Glu Arg
420 425 430

Asp Trp Gly Val Gln Gln Leu Val Thr Ser Ala Asp Trp Gly Gly Lys
435 440 445

Ile Gly Asn Phe Phe Thr Gly Gly Leu Asn Leu Gln Val Glu His His
450 455 460

Leu Phe Pro Ala Ile Cys Phe Val His Tyr Pro Asp Ile Ala Lys Ile
465 470 475 480

Val Lys Glu Glu Ala Ala Lys Leu Asn Ile Pro Tyr Ala Ser Tyr Arg
485 490 495

Thr Leu Pro Gly Ile Phe Val Gln Phe Trp Arg Phe Met Lys Asp Met
500 505 510

Gly Thr Ala Glu Gln Ile Gly Glu Val Pro Leu Pro Lys Ile Pro Asn
515 520 525

Pro Gln Leu Ala Pro Lys Leu Ala
530 535

<210> 97
<211> 1455
<212> DNA
<213> *Thalassiosira pseudonana*

<220>
<221> CDS
<222> (1)..(1455)
<223> Delta-6-Desaturase

<400> 97
atg gga aaa gga gga gac gca gcc gca gct acc aag cgt agt gga gca 48
Met Gly Lys Gly Gly Asp Ala Ala Ala Thr Lys Arg Ser Gly Ala
1 5 10 15
ttg aaa ttg gcg gag aag ccg cag aag tac act tgg cag gag gtg aag 96
Leu Lys Leu Ala Glu Lys Pro Gln Lys Tyr Thr Trp Gln Glu Val Lys
20 25 30
aag cac atc acc ccc gac gat gcc tgg gta gtc cac caa aac aaa gtc 144
Lys His Ile Thr Pro Asp Asp Ala Trp Val Val His Gln Asn Lys Val
35 40 45
tac gac gtc tcc aac tgg tac gac cac ccc ggt gga gcc gtg gtg ttc 192
Tyr Asp Val Ser Asn Trp Tyr Asp His Pro Gly Gly Ala Val Val Phe
50 55 60
acc cac gcc gga gac gac atg acg gac atc ttc gcc gcc ttc cac gcc 240
Thr His Ala Gly Asp Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala
65 70 75 80
caa ggc tct cag gcc atg atg aag aag ttt tac att gga gat ttg att 288
Gln Gly Ser Gln Ala Met Met Lys Lys Phe Tyr Ile Gly Asp Leu Ile

95

ccg	gag	agt	gtg	gag	cat	aag	gat	caa	aga	cag	ttg	gat	ttc	gag	aag	336
Pro	Glu	Ser	Val	Glu	His	Lys	Asp	Gln	Arg	Gln	Leu	Asp	Phe	Glu	Lys	
			100					105					110			
gga	tat	cgt	gat	tta	cgg	gcc	aag	ctt	gtc	atg	atg	ggg	atg	ttc	aag	384
Gly	Tyr	Arg	Asp	Leu	Arg	Ala	Lys	Leu	Val	Met	Met	Gly	Met	Phe	Lys	
		115					120					125				
tcg	agt	aag	atg	tat	tat	gca	tac	aag	tgc	tcg	ttc	aat	atg	tgc	atg	432
Ser	Ser	Lys	Met	Tyr	Tyr	Ala	Tyr	Lys	Cys	Ser	Phe	Asn	Met	Cys	Met	
	130					135					140					
tgg	ttg	gtg	gcg	gtg	gcc	atg	gtg	tac	tac	tcg	gac	agt	ttg	gca	atg	480
Trp	Leu	Val	Ala	Val	Ala	Met	Val	Tyr	Tyr	Ser	Asp	Ser	Leu	Ala	Met	
145					150					155					160	
cac	att	gga	tcg	gct	ctc	ttg	ttg	gga	ttg	ttc	tgg	cag	cag	tgt	gga	528
His	Ile	Gly	Ser	Ala	Leu	Leu	Leu	Gly	Leu	Phe	Trp	Gln	Gln	Cys	Gly	
				165					170					175		
tgg	ctt	gcg	cac	gac	ttt	ctt	cac	cac	caa	gtc	ttt	aag	caa	cga	aag	576
Trp	Leu	Ala	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Lys	Gln	Arg	Lys	
			180					185					190			
tac	gga	gat	ctc	gtt	ggc	atc	ttt	tgg	gga	gat	ctc	atg	cag	ggg	ttc	624
Tyr	Gly	Asp	Leu	Val	Gly	Ile	Phe	Trp	Gly	Asp	Leu	Met	Gln	Gly	Phe	
		195					200					205				
tcg	atg	cag	tgg	tgg	aag	aac	aag	cac	aat	ggc	cac	cat	gct	gtt	ccc	672
Ser	Met	Gln	Trp	Trp	Lys	Asn	Lys	His	Asn	Gly	His	His	Ala	Val	Pro	
	210					215					220					
aac	ttg	cac	aac	tct	tcc	ttg	gac	agt	cag	gat	ggg	gat	ccc	gat	att	720
Asn	Leu	His	Asn	Ser	Ser	Leu	Asp	Ser	Gln	Asp	Gly	Asp	Pro	Asp	Ile	
225					230					235					240	
gat	acc	atg	cca	ctc	ctt	gct	tgg	agt	ctc	aag	cag	gct	cag	agt	ttc	768
Asp	Thr	Met	Pro	Leu	Leu	Ala	Trp	Ser	Leu	Lys	Gln	Ala	Gln	Ser	Phe	
				245					250					255		
aga	gag	atc	aat	aag	gga	aag	gac	agt	acc	ttc	gtc	aag	tac	gct	atc	816
Arg	Glu	Ile	Asn	Lys	Gly	Lys	Asp	Ser	Thr	Phe	Val	Lys	Tyr	Ala	Ile	
			260					265					270			
aaa	ttc	cag	gca	ttc	aca	tac	ttc	ccc	atc	ctc	ctc	ttg	gct	cgc	atc	864
Lys	Phe	Gln	Ala	Phe	Thr	Tyr	Phe	Pro	Ile	Leu	Leu	Leu	Ala	Arg	Ile	
		275					280					285				
tct	tgg	ttg	aat	gaa	tcc	ttc	aaa	act	gca	ttc	gga	ctc	gga	gct	gcc	912
Ser	Trp	Leu	Asn	Glu	Ser	Phe	Lys	Thr	Ala	Phe	Gly	Leu	Gly	Ala	Ala	
	290					295					300					
tcg	gag	aat	gcc	aag	ttg	gag	ttg	gag	aag							

153

355	360	365	
gga ttg gga cac aac ggt atg tca gtg tac gat gcc acc acc cga cct Gly Leu Gly His Asn Gly Met Ser Val Tyr Asp Ala Thr Thr Arg Pro 370 375 380			1152
gac ttc tgg caa ctc caa gtc acc act aca cgt aac atc att ggt gga Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Ile Gly Gly 385 390 395 400			1200
cac ggc att ccc caa ttc ttt gtg gat tgg ttc tgc ggt gga ttg caa His Gly Ile Pro Gln Phe Phe Val Asp Trp Phe Cys Gly Gly Leu Gln 405 410 415			1248
tac caa gtg gat cac cac ctc ttc ccc atg atg cct aga aac aat atc Tyr Gln Val Asp His His Leu Phe Pro Met Met Pro Arg Asn Asn Ile 420 425 430			1296
gcg aaa tgc cac aag ctt gtg gag tca ttc tgt aag gag tgg ggt gtg Ala Lys Cys His Lys Leu Val Glu Ser Phe Cys Lys Glu Trp Gly Val 435 440 445			1344
aag tac cat gag gcc gat atg tgg gat ggt acc gtg gaa gtg ttg caa Lys Tyr His Glu Ala Asp Met Trp Asp Gly Thr Val Glu Val Leu Gln 450 455 460			1392
cat ctc tcc aag gtg tcg gat gat ttc ctt gtg gag atg gtg aag gat His Leu Ser Lys Val Ser Asp Asp Phe Leu Val Glu Met Val Lys Asp 465 470 475 480			1440
ttc cct gcc atg taa Phe Pro Ala Met			1455

<210> 98
 <211> 484
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 98

Met Gly Lys Gly Gly Asp Ala Ala Ala Ala Thr Lys Arg Ser Gly Ala 1 5 10 15
Leu Lys Leu Ala Glu Lys Pro Gln Lys Tyr Thr Trp Gln Glu Val Lys 20 25 30
Lys His Ile Thr Pro Asp Asp Ala Trp Val Val His Gln Asn Lys Val 35 40 45
Tyr Asp Val Ser Asn Trp Tyr Asp His Pro Gly Gly Ala Val Val Phe 50 55 60
Thr His Ala Gly Asp Asp Met Thr Asp Ile Phe Ala Ala Phe His Ala 65 70 75 80
Gln Gly Ser Gln Ala Met Met Lys Lys Phe Tyr Ile Gly Asp Leu Ile 85 90 95
Pro Glu Ser Val Glu His Lys Asp Gln Arg Gln Leu Asp Phe Glu Lys 100 105 110

Gly Tyr Arg Asp Leu Arg Ala Lys Leu Val Met Met Gly Met Phe Lys
 115 120 125

Ser Ser Lys Met Tyr Tyr Ala Tyr Lys Cys Ser Phe Asn Met Cys Met
 130 135 140

Trp Leu Val Ala Val Ala Met Val Tyr Tyr Ser Asp Ser Leu Ala Met
 145 150 155 160

His Ile Gly Ser Ala Leu Leu Leu Gly Leu Phe Trp Gln Gln Cys Gly
 165 170 175

Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Lys Gln Arg Lys
 180 185 190

Tyr Gly Asp Leu Val Gly Ile Phe Trp Gly Asp Leu Met Gln Gly Phe
 195 200 205

Ser Met Gln Trp Trp Lys Asn Lys His Asn Gly His His Ala Val Pro
 210 215 220

Asn Leu His Asn Ser Ser Leu Asp Ser Gln Asp Gly Asp Pro Asp Ile
 225 230 235 240

Asp Thr Met Pro Leu Leu Ala Trp Ser Leu Lys Gln Ala Gln Ser Phe
 245 250 255

Arg Glu Ile Asn Lys Gly Lys Asp Ser Thr Phe Val Lys Tyr Ala Ile
 260 265 270

Lys Phe Gln Ala Phe Thr Tyr Phe Pro Ile Leu Leu Leu Ala Arg Ile
 275 280 285

Ser Trp Leu Asn Glu Ser Phe Lys Thr Ala Phe Gly Leu Gly Ala Ala
 290 295 300

Ser Glu Asn Ala Lys Leu Glu Leu Glu Lys Arg Gly Leu Gln Tyr Pro
 305 310 315 320

Leu Leu Glu Lys Leu Gly Ile Thr Leu His Tyr Thr Trp Met Phe Val
 325 330 335

Leu Ser Ser Gly Phe Gly Arg Trp Ser Leu Pro Tyr Ser Ile Met Tyr
 340 345 350

Phe Phe Thr Ala Thr Cys Ser Ser Gly Leu Phe Leu Ala Leu Val Phe
 355 360 365

Gly Leu Gly His Asn Gly Met Ser Val Tyr Asp Ala Thr Thr Arg Pro
 370 375 380

Asp Phe Trp Gln Leu Gln Val Thr Thr Thr Arg Asn Ile Ile Gly Gly
385 390 395 400

His Gly Ile Pro Gln Phe Phe Val Asp Trp Phe Cys Gly Gly Leu Gln
405 410 415

Tyr Gln Val Asp His His Leu Phe Pro Met Met Pro Arg Asn Asn Ile
420 425 430

Ala Lys Cys His Lys Leu Val Glu Ser Phe Cys Lys Glu Trp Gly Val
435 440 445

Lys Tyr His Glu Ala Asp Met Trp Asp Gly Thr Val Glu Val Leu Gln
450 455 460

His Leu Ser Lys Val Ser Asp Asp Phe Leu Val Glu Met Val Lys Asp
465 470 475 480

Phe Pro Ala Met

<210> 99
<211> 1431
<212> DNA
<213> *Thalassiosira pseudonana*

<220>
<221> CDS
<222> (1)..(1431)
<223> Delta-5-Desaturase

<400> 99
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Met Pro Pro Asn Ala Asp Ile Ser Arg Ile Arg Asn Arg Ile Pro Thr
1 5 10 15

aaa aca ggt acc gtt gcc tct gcc gac aac aac gac ccc gcc acc caa 96
Lys Thr Gly Thr Val Ala Ser Ala Asp Asn Asn Asp Pro Ala Thr Gln
20 25 30

tcc gtc cga acc ctc aaa tct ctc aag ggc aac gag gtc gtc atc aac 144
Ser Val Arg Thr Leu Lys Ser Leu Lys Gly Asn Glu Val Val Ile Asn
35 40 45

ggc aca att tat gac att gct gac ttt gtc cat cct gga gga gag gtt 192
Gly Thr Ile Tyr Asp Ile Ala Asp Phe Val His Pro Gly Gly Glu Val
50 55 60

gtc aag ttc ttt ggt ggg aat gat gtt act att cag tat aat atg att 240
Val Lys Phe Phe Gly Gly Asn Asp Val Thr Ile Gln Tyr Asn Met Ile
65 70 75 80

cat ccg tat cat acg ggg aaa cat ctg gag aag atg aag gct gtt gga 288
His Pro Tyr His Thr Gly Lys His Leu Glu Lys Met Lys Ala Val Gly
85 90 95

aag gtt gta gat tgg cag tcg gac tac aag ttc gac acc ccc ttt gaa 336
Lys Val Val Asp Trp Gln Ser Asp Tyr Lys Phe Asp Thr Pro Phe Glu

156

100	105	110	
cga gag atc aaa tca gaa gtg ttc aag atc gta cgt cgc ggg cgt gag Arg Glu Ile Lys Ser Glu Val Phe Lys Ile Val Arg Arg Gly Arg Glu 115 120 125			384
ttc ggc aca aca ggc tac ttc ctc cgt gcc ttt ttc tac atc gct ctc Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala Phe Phe Tyr Ile Ala Leu 130 135 140			432
ttc ttc acc atg caa tac act ttc gcc aca tgc acc acc ttc acc acc Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr Cys Thr Thr Phe Thr Thr 145 150 155 160			480
tac gat cac tgg tat cag agt ggt gta ttc atc gca att gtg ttt ggt Tyr Asp His Trp Tyr Gln Ser Gly Val Phe Ile Ala Ile Val Phe Gly 165 170 175			528
att tca cag gca ttc att ggg ttg aat gtc cag cac gat gcc aat cac Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His 180 185 190			576
gga gct gcc agt aag cgt ccc tgg gtg aat gac ttg ttg gga ttt gga Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly 195 200 205			624
acg gat ttg att gga tct aac aaa tgg aat tgg atg gca cag cat tgg Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp 210 215 220			672
act cat cac gct tac act aac cat agt gag aag gat ccc gat agc ttc Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe 225 230 235 240			720
agc tcg gaa cct atg ttt gca ttc aat gac tat ccc att gga cac ccg Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro 245 250 255			768
aag aga aag tgg tgg cat agg ttc cag gga ggg tac ttc ctc ttc atg Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met 260 265 270			816
ctt gga ctt tac tgg ctc tcg act gta ttc aat ccg caa ttc att gat Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp 275 280 285			864
ctt cgt caa cgt ggg gct cag tac gtc gga att caa atg gag aat gat Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp 290 295 300			912
ttc att gtc aag agg agg aag tac gcc gtt gca ttg agg atg atg tac Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr 305 310 315 320			960
att tac ttg aac att gtc agc ccc ttc atg aac aat ggt ttg agc tgg Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp 325 330 335			1008
tct acc ttt gga atc atc atg ttg atg gga atc agc gag agt ctc act Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr 340 345 350			1056
ctc agt gtg ctc ttc tcg ttg tct cac aac ttc atc aat tcg gat cgt Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg 355 360 365			1104
gat cct acg gct gac ttc aaa aag acc gga gaa caa gtg tgc tgg ttc Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe			1152

157

370	375	380	
aag tcg cag gtg gag act tcg tct acc tat ggg ggt ttt att tcc gga			1200
Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly			
385	390	395	400
tgt ctt acg gga gga ctc aac ttt cag gtg gaa cat cat ctc ttt ccc			1248
Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro			
	405	410	415
cgt atg agc agt gct tgg tat cct tac att gca cct acg gtt cgt gag			1296
Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu			
	420	425	430
gtt tgc aag aag cac ggg gtg aac tac gct tat tat cct tgg att ggg			1344
Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly			
	435	440	445
cag aat ttg gta tca aca ttc aaa tac atg cat cgc gct ggt agt gga			1392
Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly			
	450	455	460
gcc aac tgg gag ctc aag ccg ttg tct gga agt gcc taa			1431
Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala			
465	470	475	
<210>	100		
<211>	476		
<212>	PRT		
<213>	Thalassiosira pseudonana		
<400>	100		
Met Pro Pro Asn Ala Asp Ile Ser Arg Ile Arg Asn Arg Ile Pro Thr			
1	5	10	15
Lys Thr Gly Thr Val Ala Ser Ala Asp Asn Asn Asp Pro Ala Thr Gln			
	20	25	30
Ser Val Arg Thr Leu Lys Ser Leu Lys Gly Asn Glu Val Val Ile Asn			
	35	40	45
Gly Thr Ile Tyr Asp Ile Ala Asp Phe Val His Pro Gly Gly Glu Val			
	50	55	60
Val Lys Phe Phe Gly Gly Asn Asp Val Thr Ile Gln Tyr Asn Met Ile			
65	70	75	80
His Pro Tyr His Thr Gly Lys His Leu Glu Lys Met Lys Ala Val Gly			
	85	90	95
Lys Val Val Asp Trp Gln Ser Asp Tyr Lys Phe Asp Thr Pro Phe Glu			
	100	105	110
Arg Glu Ile Lys Ser Glu Val Phe Lys Ile Val Arg Arg Gly Arg Glu			
	115	120	125
Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala Phe Phe Tyr Ile Ala Leu			
	130	135	140

Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr Cys Thr Thr Phe Thr Thr
145 150 155 160

Tyr Asp His Trp Tyr Gln Ser Gly Val Phe Ile Ala Ile Val Phe Gly
165 170 175

Ile Ser Gln Ala Phe Ile Gly Leu Asn Val Gln His Asp Ala Asn His
180 185 190

Gly Ala Ala Ser Lys Arg Pro Trp Val Asn Asp Leu Leu Gly Phe Gly
195 200 205

Thr Asp Leu Ile Gly Ser Asn Lys Trp Asn Trp Met Ala Gln His Trp
210 215 220

Thr His His Ala Tyr Thr Asn His Ser Glu Lys Asp Pro Asp Ser Phe
225 230 235 240

Ser Ser Glu Pro Met Phe Ala Phe Asn Asp Tyr Pro Ile Gly His Pro
245 250 255

Lys Arg Lys Trp Trp His Arg Phe Gln Gly Gly Tyr Phe Leu Phe Met
260 265 270

Leu Gly Leu Tyr Trp Leu Ser Thr Val Phe Asn Pro Gln Phe Ile Asp
275 280 285

Leu Arg Gln Arg Gly Ala Gln Tyr Val Gly Ile Gln Met Glu Asn Asp
290 295 300

Phe Ile Val Lys Arg Arg Lys Tyr Ala Val Ala Leu Arg Met Met Tyr
305 310 315 320

Ile Tyr Leu Asn Ile Val Ser Pro Phe Met Asn Asn Gly Leu Ser Trp
325 330 335

Ser Thr Phe Gly Ile Ile Met Leu Met Gly Ile Ser Glu Ser Leu Thr
340 345 350

Leu Ser Val Leu Phe Ser Leu Ser His Asn Phe Ile Asn Ser Asp Arg
355 360 365

Asp Pro Thr Ala Asp Phe Lys Lys Thr Gly Glu Gln Val Cys Trp Phe
370 375 380

Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr Gly Gly Phe Ile Ser Gly
385 390 395 400

Cys Leu Thr Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro
405 410 415

Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Thr Val Arg Glu
 420 425 430

Val Cys Lys Lys His Gly Val Asn Tyr Ala Tyr Tyr Pro Trp Ile Gly
 435 440 445

Gln Asn Leu Val Ser Thr Phe Lys Tyr Met His Arg Ala Gly Ser Gly
 450 455 460

Ala Asn Trp Glu Leu Lys Pro Leu Ser Gly Ser Ala
 465 470 475

<210> 101
 <211> 1449
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(1449)
 <223> Delta-5-Desaturase

<400> 101
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 Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro
 1 5 10 15
 acg aag aag tcc agt tca tcg tca tcc acc gcg aac gac gat ccg gct 96
 Thr Lys Lys Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala
 20 25 30
 acc caa tcc acc tca cct gtg aac cga acc ctc aag tct ttg aat gga 144
 Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly
 35 40 45
 aac gaa ata gct att gac ggt gtc atc tat gat att gat ggc ttt gtc 192
 Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val
 50 55 60
 cat cct gga gga gag gtt att agc ttc ttt gga ggc aac gat gtg act 240
 His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr
 65 70 75 80
 gta cag tac aaa atg att cat ccg tat cat aat agt aag cat ctc gag 288
 Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu
 85 90 95
 aag atg aga gcc gtt gga aag att gca gac tac tcc aca gag tac aag 336
 Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys
 100 105 110
 ttc gac aca ccc ttt gaa cga gag atc aaa tcc gaa gtg ttc aaa atc 384
 Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile
 115 120 125
 gtc cgt cga gga cgt gaa ttc ggt aca aca gga tat ttc ctc cgt gcc 432
 Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala
 130 135 140
 ttc ttc tac att gct ctc ttc ttc acc atg caa tac acc ttc gcc aca 480
 Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr

160

145	150	155	160	
tgc act acc ttc acc acc tac gat cat tgg tat caa agt ggt gta ttc Cys Thr Thr Phe Thr Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe 165 170 175				528
atc gcc att gtg ttt ggt atc tca caa gct ttc att ggg ttg aat gta Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val 180 185 190				576
caa cat gat gcc aat cac gga gct gct agc aaa cga cct tgg gtg aat Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn 195 200 205				624
gat ctc ctt gga tct gga gct gat ctc atc ggt gga tgc aaa tgg aac Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn 210 215 220				672
tgg ttg gct cag cat tgg act cat cat gcg tat acc aat cac gct gat Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp 225 230 235 240				720
aaa gat cct gat agc ttt agt tcc gag ccg gtc ttc aac ttt aac gat Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp 245 250 255				768
tat ccc att ggt cac ccc aaa aga aag tgg tgg cat agg ttc caa ggg Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly 260 265 270				816
ctc tac ttc cta atc atg ctg agt ttc tat tgg gta tcg atg gta ttc Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe 275 280 285				864
aac cca caa gtt atc gac ctc cgt cat gct gga gct gcc tac gtt gga Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly 290 295 300				912
ttt cag atg gag aac gac ttt atc gtc aaa cgg aga aag tat gca atg Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met 305 310 315 320				960
gca ctt cgt gca atg tac ttc tat ttc aac atc tat tgt ccg att gtc Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val 325 330 335				1008
aac aat gga ttg act tgg tcg aca gtt gga atc atc ctc tta atg gga Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly 340 345 350				1056
gtt agc gaa agc ttc atg ctc tcc ggt cta ttc gta ctc tca cac aac Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn 355 360 365				1104
ttt gaa aat tcc gaa cgt gat cct acc tct gag tat cgc aag act ggt Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly 370 375 380				1152
gag caa gta tgt tgg ttc aag tct caa gtg gag act tct tct acc tac Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr 385 390 395 400				1200
gga ggt atc gtt gct ggg tgt ctc act ggt gga ctc aac ttt caa gtg Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val 405 410 415				1248
gag cat cat ttg ttc ccg agg atg agc agt gct tgg tat cct ttc atc Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile				1296

161

420	425	430	
gcg ccg aag gtt aga gag att tgt aag aag cat gga gtt aga tac gct Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala 435 440 445			1344
tac tat ccg tac atc tgg cag aac ttg cat tct acc gtg agt tac atg Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met 450 455 460			1392
cat ggg acg gga acg gga gct aga tgg gag ctt cag ccg ttg tct gga His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly 465 470 475 480			1440
agg gcg tag Arg Ala			1449

<210> 102
 <211> 482
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 102

Met Pro Pro Asn Ala Glu Val Lys Asn Leu Arg Ser Arg Ser Ile Pro 1 5 10 15
Thr Lys Lys Ser Ser Ser Ser Ser Ser Thr Ala Asn Asp Asp Pro Ala 20 25 30
Thr Gln Ser Thr Ser Pro Val Asn Arg Thr Leu Lys Ser Leu Asn Gly 35 40 45
Asn Glu Ile Ala Ile Asp Gly Val Ile Tyr Asp Ile Asp Gly Phe Val 50 55 60
His Pro Gly Gly Glu Val Ile Ser Phe Phe Gly Gly Asn Asp Val Thr 65 70 75 80
Val Gln Tyr Lys Met Ile His Pro Tyr His Asn Ser Lys His Leu Glu 85 90 95
Lys Met Arg Ala Val Gly Lys Ile Ala Asp Tyr Ser Thr Glu Tyr Lys 100 105 110
Phe Asp Thr Pro Phe Glu Arg Glu Ile Lys Ser Glu Val Phe Lys Ile 115 120 125
Val Arg Arg Gly Arg Glu Phe Gly Thr Thr Gly Tyr Phe Leu Arg Ala 130 135 140
Phe Phe Tyr Ile Ala Leu Phe Phe Thr Met Gln Tyr Thr Phe Ala Thr 145 150 155 160
Cys Thr Thr Phe Thr Thr Tyr Asp His Trp Tyr Gln Ser Gly Val Phe 165 170 175

Ile Ala Ile Val Phe Gly Ile Ser Gln Ala Phe Ile Gly Leu Asn Val
 180 185 190

Gln His Asp Ala Asn His Gly Ala Ala Ser Lys Arg Pro Trp Val Asn
 195 200 205

Asp Leu Leu Gly Ser Gly Ala Asp Leu Ile Gly Gly Cys Lys Trp Asn
 210 215 220

Trp Leu Ala Gln His Trp Thr His His Ala Tyr Thr Asn His Ala Asp
 225 230 235 240

Lys Asp Pro Asp Ser Phe Ser Ser Glu Pro Val Phe Asn Phe Asn Asp
 245 250 255

Tyr Pro Ile Gly His Pro Lys Arg Lys Trp Trp His Arg Phe Gln Gly
 260 265 270

Leu Tyr Phe Leu Ile Met Leu Ser Phe Tyr Trp Val Ser Met Val Phe
 275 280 285

Asn Pro Gln Val Ile Asp Leu Arg His Ala Gly Ala Ala Tyr Val Gly
 290 295 300

Phe Gln Met Glu Asn Asp Phe Ile Val Lys Arg Arg Lys Tyr Ala Met
 305 310 315 320

Ala Leu Arg Ala Met Tyr Phe Tyr Phe Asn Ile Tyr Cys Pro Ile Val
 325 330 335

Asn Asn Gly Leu Thr Trp Ser Thr Val Gly Ile Ile Leu Leu Met Gly
 340 345 350

Val Ser Glu Ser Phe Met Leu Ser Gly Leu Phe Val Leu Ser His Asn
 355 360 365

Phe Glu Asn Ser Glu Arg Asp Pro Thr Ser Glu Tyr Arg Lys Thr Gly
 370 375 380

Glu Gln Val Cys Trp Phe Lys Ser Gln Val Glu Thr Ser Ser Thr Tyr
 385 390 395 400

Gly Gly Ile Val Ala Gly Cys Leu Thr Gly Gly Leu Asn Phe Gln Val
 405 410 415

Glu His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Phe Ile
 420 425 430

Ala Pro Lys Val Arg Glu Ile Cys Lys Lys His Gly Val Arg Tyr Ala
 435 440 445

Tyr Tyr Pro Tyr Ile Trp Gln Asn Leu His Ser Thr Val Ser Tyr Met
 450 455 460

His Gly Thr Gly Thr Gly Ala Arg Trp Glu Leu Gln Pro Leu Ser Gly
 465 470 475 480

Arg Ala

<210> 103
 <211> 1512
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(1512)
 <223> Delta-4-Desaturase

<400> 103
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 Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr
 1 5 10 15
 tcg aag ccc cag cag caa cat gag cat cgc acc atc tcc aag tcc gag 96
 Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu
 20 25 30
 ctc gcc caa cac aac acg ccc aaa tca gca tgg tgt gcc gtc cac tcc 144
 Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser
 35 40 45
 act ccc gcc acc gac cca tcc cac tcc aac aac aaa caa cac gca cac 192
 Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His
 50 55 60
 cta gtc ctc gac att acc gac ttt gcg tcc cgc cat cca ggg gga gac 240
 Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp
 65 70 75 80
 ctc atc ctc ctc gct tcc ggc aaa gac gcc tcg gtg ctg ttt gaa aca 288
 Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr
 85 90 95
 tac cat cca cgt gga gtt ccg acg tct ctc att caa aag ctg cag att 336
 Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile
 100 105 110
 gga gtg atg gag gag gag gcg ttt cgg gat tcg ttt tac agt tgg act 384
 Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr
 115 120 125
 gat tct gac ttt tat act gtg ttg aag agg agg gtt gtg gag cgg ttg 432
 Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu
 130 135 140
 gag gag agg ggg ttg gac agg agg gga tcg aaa gag att tgg atc aag 480
 Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys
 145 150 155 160
 gct ttg ttc ttg ttg gtt gga ttt tgg tac tgt ttg tac aag atg tat 528
 Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr

164

165	170	175	
act acg tcg gat atc gat cag tac ggt att gcc att gcc tat tct att Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile 180 185 190			576
gga atg gga acc ttt gcg gca ttc atc ggc acg tgt att caa cac gat Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp 195 200 205			624
gga aat cac ggt gca ttc gct cag aac aag tta ctc aac aag ttg gct Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala 210 215 220			672
ggg tgg acg ttg gat atg att ggt gcg agt gcg ttt acg tgg gag ctt Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu 225 230 235 240			720
cag cac atg ctg ggg cat cat cca tat acg aat gtg ttg gat ggg gtg Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val 245 250 255			768
gag gag gag agg aag gag agg ggg gag gat gtt gct ttg gaa gaa aag Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys 260 265 270			816
gat cag gat ttt gaa gtt gcc aca tcc gga cga tta tat cat att gat Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp 275 280 285			864
gcc aat gta cgt tat ggt tcg gta tgg aat gtc atg agg ttt tgg gct Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala 290 295 300			912
atg aag gtc att acg atg gga tat atg atg gga tta cca atc tac ttt Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe 305 310 315 320			960
cat gga gta ctg agg gga gtt gga ttg ttt gtt att ggg cat ttg gcg His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala 325 330 335			1008
tgt gga gag ttg ttg gcg acg atg ttt att gtg aat cac gtc att gag Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu 340 345 350			1056
ggt gtg agt tat gga acg aag gat ttg gtt ggt ggt gcg agt cat gta Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val 355 360 365			1104
gat gag aag aag att gtc aag cca acg act gta ttg gga gat aca cca Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro 370 375 380			1152
atg gta aag act cgc gag gag gca ttg aaa agc aac agc aat aac aac Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn 385 390 395 400			1200
aag aag aag gga gag aag aac tcg gta cca tcc gtt cca ttc aac gac Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp 405 410 415			1248
tgg gca gca gtc caa tgc cag acc tcc gtg aat tgg tct cca ggc tca Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser 420 425 430			1296
tgg ttc tgg aat cac ttt tct ggg gga ctc tct cat cag att gag cat Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His			1344

165

435	440	445	
cac ttg ttc ccc agc att tgt cat aca aac tac tgt cat atc cag gat			1392
His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp			
450	455	460	
gtt gtg gag agt acg tgt gct gag tac gga gtt ccg tat cag agt gag			1440
Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu			
465	470	475	480
agt aat ttg ttt gtt gct tat gga aag atg att agt cat ttg aag ttt			1488
Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe			
485	490	495	
ttg ggt aaa gcc aag tgt gag tag			1512
Leu Gly Lys Ala Lys Cys Glu			
500			

<210> 104
 <211> 503
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 104

Met Cys Asn Gly Asn Leu Pro Ala Ser Thr Ala Gln Leu Lys Ser Thr			
1	5	10	15
Ser Lys Pro Gln Gln Gln His Glu His Arg Thr Ile Ser Lys Ser Glu			
	20	25	30
Leu Ala Gln His Asn Thr Pro Lys Ser Ala Trp Cys Ala Val His Ser			
35	40	45	
Thr Pro Ala Thr Asp Pro Ser His Ser Asn Asn Lys Gln His Ala His			
50	55	60	
Leu Val Leu Asp Ile Thr Asp Phe Ala Ser Arg His Pro Gly Gly Asp			
65	70	75	80
Leu Ile Leu Leu Ala Ser Gly Lys Asp Ala Ser Val Leu Phe Glu Thr			
85	90	95	
Tyr His Pro Arg Gly Val Pro Thr Ser Leu Ile Gln Lys Leu Gln Ile			
100	105	110	
Gly Val Met Glu Glu Glu Ala Phe Arg Asp Ser Phe Tyr Ser Trp Thr			
115	120	125	
Asp Ser Asp Phe Tyr Thr Val Leu Lys Arg Arg Val Val Glu Arg Leu			
130	135	140	
Glu Glu Arg Gly Leu Asp Arg Arg Gly Ser Lys Glu Ile Trp Ile Lys			
145	150	155	160
Ala Leu Phe Leu Leu Val Gly Phe Trp Tyr Cys Leu Tyr Lys Met Tyr			
165	170	175	

Thr Thr Ser Asp Ile Asp Gln Tyr Gly Ile Ala Ile Ala Tyr Ser Ile
 180 185 190

Gly Met Gly Thr Phe Ala Ala Phe Ile Gly Thr Cys Ile Gln His Asp
 195 200 205

Gly Asn His Gly Ala Phe Ala Gln Asn Lys Leu Leu Asn Lys Leu Ala
 210 215 220

Gly Trp Thr Leu Asp Met Ile Gly Ala Ser Ala Phe Thr Trp Glu Leu
 225 230 235 240

Gln His Met Leu Gly His His Pro Tyr Thr Asn Val Leu Asp Gly Val
 245 250 255

Glu Glu Glu Arg Lys Glu Arg Gly Glu Asp Val Ala Leu Glu Glu Lys
 260 265 270

Asp Gln Asp Phe Glu Val Ala Thr Ser Gly Arg Leu Tyr His Ile Asp
 275 280 285

Ala Asn Val Arg Tyr Gly Ser Val Trp Asn Val Met Arg Phe Trp Ala
 290 295 300

Met Lys Val Ile Thr Met Gly Tyr Met Met Gly Leu Pro Ile Tyr Phe
 305 310 315 320

His Gly Val Leu Arg Gly Val Gly Leu Phe Val Ile Gly His Leu Ala
 325 330 335

Cys Gly Glu Leu Leu Ala Thr Met Phe Ile Val Asn His Val Ile Glu
 340 345 350

Gly Val Ser Tyr Gly Thr Lys Asp Leu Val Gly Gly Ala Ser His Val
 355 360 365

Asp Glu Lys Lys Ile Val Lys Pro Thr Thr Val Leu Gly Asp Thr Pro
 370 375 380

Met Val Lys Thr Arg Glu Glu Ala Leu Lys Ser Asn Ser Asn Asn Asn
 385 390 395 400

Lys Lys Lys Gly Glu Lys Asn Ser Val Pro Ser Val Pro Phe Asn Asp
 405 410 415

Trp Ala Ala Val Gln Cys Gln Thr Ser Val Asn Trp Ser Pro Gly Ser
 420 425 430

Trp Phe Trp Asn His Phe Ser Gly Gly Leu Ser His Gln Ile Glu His
 435 440 445

His Leu Phe Pro Ser Ile Cys His Thr Asn Tyr Cys His Ile Gln Asp
 450 455 460

Val Val Glu Ser Thr Cys Ala Glu Tyr Gly Val Pro Tyr Gln Ser Glu
 465 470 475 480

Ser Asn Leu Phe Val Ala Tyr Gly Lys Met Ile Ser His Leu Lys Phe
 485 490 495

Leu Gly Lys Ala Lys Cys Glu
 500

<210> 105
 <211> 1257
 <212> DNA
 <213> *Thalassiosira pseudonana*

<220>
 <221> CDS
 <222> (1)..(1257)
 <223> Omega-3-Desaturase

<400> 105
 atg tac aga tta aca tcc acc ttc ctc atc gca ttg gca ttc tcc tcc 48
 Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser
 1 5 10 15
 tcc atc aat gcc ttc tct cca caa cgg cca cca cgt act atc acc aaa 96
 Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys
 20 25 30
 agt aaa gtc caa agc acc gtg cta ccc ata ccg acc aag gat gat ctg 144
 Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu
 35 40 45
 aac ttt ctc caa cca caa ctc gat gag aat gat ctc tac ctc gac gat 192
 Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp
 50 55 60
 gtc aac act cca cca aga gca ggt acc atc atg aag atg ttg ccg aag 240
 Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys
 65 70 75 80
 gaa acg ttc aac att gat aca gca act tca ttg ggt tac ttt ggt atg 288
 Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met
 85 90 95
 gat atg gca gcg gtt gta tcg tcc atg acg ttg cta aat gct att gta 336
 Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val
 100 105 110
 act tcg gat cag tac cat gct ctt cca ctt cct ctc caa gca gca aca 384
 Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr
 115 120 125
 gtg att ccc ttt cag cta ttg gct ggg ttc gcc atg tgg tgt atg tgg 432
 Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp
 130 135 140
 tgc att gga cac gat gct gga cat tct act gtt tcg aag aca aag tgg 480
 Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp

168

145	150	155	160	
atc aac cga gtc gtt ggt gaa gtg gct cat tct gtt gtt tgt ctc acg Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr 165 170 175				528
ccg ttc gtg cct tgg cag atg tcg cat agg aaa cac cat ttg aat cac Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His 180 185 190				576
aat cat att gaa aag gac tac tct cat aag tgg tac agt cgc gac gag Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu 195 200 205				624
ttt gat gat atc cca caa ctc tat aag aca ttt ggc tac aac cca aga Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg 210 215 220				672
atg atg caa ctt cca ttc ctc tac ttc atg tat ctt gca ttg gga att Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile 225 230 235 240				720
cca gat ggt ggg cat gtt gtg ttc tac gga aga atg tgg gaa gga gtg Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val 245 250 255				768
tca ttg cag aag aag ttt gat gct gct att tct gtg gcc gta tca tgt Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys 260 265 270				816
gca act gct gga tcg ctt tgg atg aat atg ggt aca gca gac ttc acg Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr 275 280 285				864
gtg gta tgc atg gtt cct tgg cta gtt cta tcg tgg tgg ctc ttc atg Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met 290 295 300				912
gta aca tac ctt cag cat cat tca gaa gac gga aag cta tac act gat Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp 305 310 315 320				960
gaa acg ttt aca ttt gaa aag gga gcc ttc gag acc gtg gat cgt tcg Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser 325 330 335				1008
tac ggc aag ttg atc aac cga atg tcg cat cac atg atg gac ggt cac Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His 340 345 350				1056
gtg gtg cac cac ttg ttc ttt gaa cgt gta cct cac tac aga tta gag Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu 355 360 365				1104
gca gct acc gaa gct ctt gtg aaa gga atg gat gaa acg gga cag aaa Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys 370 375 380				1152
cat ttg tac aaa tac att gat act cct gat ttc aat gcc gag att gtc His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val 385 390 395 400				1200
aac gga ttt cgc gac aat tgg ttc ctt gtt gaa gag gag aac atc aaa Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys 405 410 415				1248
agg gag tag Arg Glu				1257

<210> 106
 <211> 418
 <212> PRT
 <213> *Thalassiosira pseudonana*

<400> 106

Met Tyr Arg Leu Thr Ser Thr Phe Leu Ile Ala Leu Ala Phe Ser Ser
 1 5 10 15

Ser Ile Asn Ala Phe Ser Pro Gln Arg Pro Pro Arg Thr Ile Thr Lys
 20 25 30

Ser Lys Val Gln Ser Thr Val Leu Pro Ile Pro Thr Lys Asp Asp Leu
 35 40 45

Asn Phe Leu Gln Pro Gln Leu Asp Glu Asn Asp Leu Tyr Leu Asp Asp
 50 55 60

Val Asn Thr Pro Pro Arg Ala Gly Thr Ile Met Lys Met Leu Pro Lys
 65 70 75 80

Glu Thr Phe Asn Ile Asp Thr Ala Thr Ser Leu Gly Tyr Phe Gly Met
 85 90 95

Asp Met Ala Ala Val Val Ser Ser Met Thr Leu Leu Asn Ala Ile Val
 100 105 110

Thr Ser Asp Gln Tyr His Ala Leu Pro Leu Pro Leu Gln Ala Ala Thr
 115 120 125

Val Ile Pro Phe Gln Leu Leu Ala Gly Phe Ala Met Trp Cys Met Trp
 130 135 140

Cys Ile Gly His Asp Ala Gly His Ser Thr Val Ser Lys Thr Lys Trp
 145 150 155 160

Ile Asn Arg Val Val Gly Glu Val Ala His Ser Val Val Cys Leu Thr
 165 170 175

Pro Phe Val Pro Trp Gln Met Ser His Arg Lys His His Leu Asn His
 180 185 190

Asn His Ile Glu Lys Asp Tyr Ser His Lys Trp Tyr Ser Arg Asp Glu
 195 200 205

Phe Asp Asp Ile Pro Gln Leu Tyr Lys Thr Phe Gly Tyr Asn Pro Arg
 210 215 220

Met Met Gln Leu Pro Phe Leu Tyr Phe Met Tyr Leu Ala Leu Gly Ile
 225 230 235 240

Pro Asp Gly Gly His Val Val Phe Tyr Gly Arg Met Trp Glu Gly Val
 245 250 255

Ser Leu Gln Lys Lys Phe Asp Ala Ala Ile Ser Val Ala Val Ser Cys
 260 265 270

Ala Thr Ala Gly Ser Leu Trp Met Asn Met Gly Thr Ala Asp Phe Thr
 275 280 285

Val Val Cys Met Val Pro Trp Leu Val Leu Ser Trp Trp Leu Phe Met
 290 295 300

Val Thr Tyr Leu Gln His His Ser Glu Asp Gly Lys Leu Tyr Thr Asp
 305 310 315 320

Glu Thr Phe Thr Phe Glu Lys Gly Ala Phe Glu Thr Val Asp Arg Ser
 325 330 335

Tyr Gly Lys Leu Ile Asn Arg Met Ser His His Met Met Asp Gly His
 340 345 350

Val Val His His Leu Phe Phe Glu Arg Val Pro His Tyr Arg Leu Glu
 355 360 365

Ala Ala Thr Glu Ala Leu Val Lys Gly Met Asp Glu Thr Gly Gln Lys
 370 375 380

His Leu Tyr Lys Tyr Ile Asp Thr Pro Asp Phe Asn Ala Glu Ile Val
 385 390 395 400

Asn Gly Phe Arg Asp Asn Trp Phe Leu Val Glu Glu Glu Asn Ile Lys
 405 410 415

Arg Glu

<210> 107
 <211> 1086
 <212> DNA
 <213> *Ostreococcus tauri*
 <220>
 <221> CDS
 <222> (1)..(1086)
 <223> Delta-12-Desaturase

<400> 107
 atg cag gag ggg gtg cga aac att ccg aac gag tgc ttt gag acg gga 48
 Met Gln Glu Gly Val Arg Asn Ile Pro Asn Glu Cys Phe Glu Thr Gly
 1 5 10 15
 cat ctt gaa aga ccc tgg cgt tcc ggc cgg tgt ggg cgc gat ccc ggt 96
 His Leu Glu Arg Pro Trp Arg Ser Gly Arg Cys Gly Arg Asp Pro Gly

171

20					25					30						
tcg	aat	tgg	ggc	gct	ggc	ttc	cgc	ttt	ttt	tcg	ctc	aag	ggg	ttt	tgg	144
Ser	Asn	Trp	Gly	Ala	Gly	Phe	Arg	Phe	Phe	Ser	Leu	Lys	Gly	Phe	Trp	
		35					40					45				
tgg	ccg	gcg	tgg	tgg	gcg	tac	gcg	ttc	gtg	acg	ggg	acg	gcg	gcc	act	192
Trp	Pro	Ala	Trp	Trp	Ala	Tyr	Ala	Phe	Val	Thr	Gly	Thr	Ala	Ala	Thr	
	50					55					60					
ggg	tgt	tgg	gtc	gcc	gcg	cac	gag	tgc	ggg	cac	ggc	gcg	ttc	agc	gat	240
Gly	Cys	Trp	Val	Ala	Ala	His	Glu	Cys	Gly	His	Gly	Ala	Phe	Ser	Asp	
65					70					75					80	
aac	aag	acg	ttg	caa	gat	gcg	gtt	gga	tac	gtg	ttg	cac	tcg	ttg	ctc	288
Asn	Lys	Thr	Leu	Gln	Asp	Ala	Val	Gly	Tyr	Val	Leu	His	Ser	Leu	Leu	
				85					90					95		
ttg	gtg	ccg	tac	ttt	tct	tgg	cag	cga	tca	cac	gcg	gtg	cat	cac	tcg	336
Leu	Val	Pro	Tyr	Phe	Ser	Trp	Gln	Arg	Ser	His	Ala	Val	His	His	Ser	
			100					105					110			
agg	acg	aat	cac	gtt	ctt	gag	ggc	gag	acg	cac	gtg	ccg	gcg	cgc	ttg	384
Arg	Thr	Asn	His	Val	Leu	Glu	Gly	Glu	Thr	His	Val	Pro	Ala	Arg	Leu	
		115					120					125				
ggg	acg	gaa	gac	gcc	aac	gtc	gtg	ttc	aag	ctt	cgc	gaa	ttg	atc	ggt	432
Gly	Thr	Glu	Asp	Ala	Asn	Val	Val	Phe	Lys	Leu	Arg	Glu	Leu	Ile	Gly	
	130					135					140					
gaa	ggg	ccg	ttc	acg	ttt	ttc	aac	ctc	gtc	ggc	gtc	ttc	gcg	ctc	gga	480
Glu	Gly	Pro	Phe	Thr	Phe	Phe	Asn	Leu	Val	Gly	Val	Phe	Ala	Leu	Gly	
145					150					155					160	
tgg	ccg	att	tac	ttg	ctc	acc	ggc	gcg	agc	ggc	gga	ccg	gtg	cgc	ggt	528
Trp	Pro	Ile	Tyr	Leu	Leu	Thr	Gly	Ala	Ser	Gly	Gly	Pro	Val	Arg	Gly	
				165					170					175		
aac	acg	aac	cac	ttc	tta	ccc	ttc	atg	ggc	gag	aaa	ggt	aag	cac	gcg	576
Asn	Thr	Asn	His	Phe	Leu	Pro	Phe	Met	Gly	Glu	Lys	Gly	Lys	His	Ala	
			180					185					190			
ctg	ttc	ccg	ggt	aag	tgg	gcg	aag	aag	gtg	tgg	cag	tct	gac	atc	ggc	624
Leu	Phe	Pro	Gly	Lys	Trp	Ala	Lys	Lys	Val	Trp	Gln	Ser	Asp	Ile	Gly	
		195					200					205				
gtt	gtt	gcc	gtc	ctg	ggc	gcg	ctc	gcg	gct	tgg	gcg	gcg	cac	agc	ggg	672
Val	Val	Ala	Val	Leu	Gly	Ala	Leu	Ala	Ala	Trp	Ala	Ala	His	Ser	Gly	
	210					215					220					
att	gcc	aca	gtg	atg	gca	ctc	tac	gtc	ggc	ccg	tac	atg	gtg	acc	aac	720
Ile	Ala	Thr	Val	Met	Ala	Leu	Tyr	Val	Gly	Pro	Tyr	Met	Val	Thr	Asn	
225					230					235					240	
ttt	tgg	ctc	gtc	ttg	tac	acg	tgg	tta	cag	cac	acc	gac	gtt	gac	gtg	768
Phe	Trp	Leu	Val	Leu	Tyr	Thr	Trp	Leu	Gln	His	Thr	Asp	Val	Asp	Val	
				245					250					255		
ccg	cac	ttc	gag	ggc	gac	gat	tgg	aac	ttg	gtc	aag	ggg	gca	ttc	atg	816
Pro	His	Phe	Glu	Gly	Asp	Asp	Trp	Asn	Leu	Val	Lys	Gly	Ala	Phe	Met	
			260					265					270			
acg	atc	gat	cgc	ccg	tac	ggc	cca	gtt	ttt	gat	ttc	ttg	cac	cac	cgc	864
Thr	Ile	Asp	Arg	Pro	Tyr	Gly	Pro	Val	Phe	Asp	Phe	Leu	His	His	Arg	
		275					280					285				
atc	ggc	agc	acg	cac	gtc	gcg	cac	cac	atc	aac	aca	cca	ttc	ccg	cat	912
Ile	Gly	Ser	Thr	His	Val	Ala	His	His	Ile	Asn	Thr	Pro	Phe	Pro	His	

290	295	300	
tac aag gct caa atg gcg acg gat gcg cta aag gag gcg tat ccc gac			960
Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp			
305	310	315	320
ctc tac ctt tac gat cca act ccg atc gcg acc gct acg tgg cgc gtg			1008
Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val			
	325	330	335
ggg agc aag tgc atc gcc gtc gtg aag aag gga gac gaa tgg gtg ttc			1056
Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe			
	340	345	350
acg gat aag caa ctc ccg gtc gcg gcg tga			1086
Thr Asp Lys Gln Leu Pro Val Ala Ala			
	355	360	

<210> 108

<211> 361

<212> PRT

<213> Ostreococcus tauri

<400> 108

Met	Gln	Glu	Gly	Val	Arg	Asn	Ile	Pro	Asn	Glu	Cys	Phe	Glu	Thr	Gly
1				5					10					15	

His	Leu	Glu	Arg	Pro	Trp	Arg	Ser	Gly	Arg	Cys	Gly	Arg	Asp	Pro	Gly
			20					25					30		

Ser	Asn	Trp	Gly	Ala	Gly	Phe	Arg	Phe	Phe	Ser	Leu	Lys	Gly	Phe	Trp
		35					40					45			

Trp	Pro	Ala	Trp	Trp	Ala	Tyr	Ala	Phe	Val	Thr	Gly	Thr	Ala	Ala	Thr
	50					55					60				

Gly	Cys	Trp	Val	Ala	Ala	His	Glu	Cys	Gly	His	Gly	Ala	Phe	Ser	Asp
65					70					75					80

Asn	Lys	Thr	Leu	Gln	Asp	Ala	Val	Gly	Tyr	Val	Leu	His	Ser	Leu	Leu
				85					90					95	

Leu	Val	Pro	Tyr	Phe	Ser	Trp	Gln	Arg	Ser	His	Ala	Val	His	His	Ser
			100					105					110		

Arg	Thr	Asn	His	Val	Leu	Glu	Gly	Glu	Thr	His	Val	Pro	Ala	Arg	Leu
		115					120					125			

Gly	Thr	Glu	Asp	Ala	Asn	Val	Val	Phe	Lys	Leu	Arg	Glu	Leu	Ile	Gly
	130					135					140				

Glu	Gly	Pro	Phe	Thr	Phe	Phe	Asn	Leu	Val	Gly	Val	Phe	Ala	Leu	Gly
145					150					155					160

Trp	Pro	Ile	Tyr	Leu	Leu	Thr	Gly	Ala	Ser	Gly	Gly	Pro	Val	Arg	Gly
				165					170					175	

Asn Thr Asn His Phe Leu Pro Phe Met Gly Glu Lys Gly Lys His Ala
180 185 190

Leu Phe Pro Gly Lys Trp Ala Lys Lys Val Trp Gln Ser Asp Ile Gly
195 200 205

Val Val Ala Val Leu Gly Ala Leu Ala Ala Trp Ala Ala His Ser Gly
210 215 220

Ile Ala Thr Val Met Ala Leu Tyr Val Gly Pro Tyr Met Val Thr Asn
225 230 235 240

Phe Trp Leu Val Leu Tyr Thr Trp Leu Gln His Thr Asp Val Asp Val
245 250 255

Pro His Phe Glu Gly Asp Asp Trp Asn Leu Val Lys Gly Ala Phe Met
260 265 270

Thr Ile Asp Arg Pro Tyr Gly Pro Val Phe Asp Phe Leu His His Arg
275 280 285

Ile Gly Ser Thr His Val Ala His His Ile Asn Thr Pro Phe Pro His
290 295 300

Tyr Lys Ala Gln Met Ala Thr Asp Ala Leu Lys Glu Ala Tyr Pro Asp
305 310 315 320

Leu Tyr Leu Tyr Asp Pro Thr Pro Ile Ala Thr Ala Thr Trp Arg Val
325 330 335

Gly Ser Lys Cys Ile Ala Val Val Lys Lys Gly Asp Glu Trp Val Phe
340 345 350

Thr Asp Lys Gln Leu Pro Val Ala Ala
355 360

<210> 109
<211> 1305
<212> DNA
<213> Thalassiosira pseudonana

<220>
<221> CDS
<222> (1)..(1305)
<223> Delta-12-Desaturase

<400> 109
atg gga aag gga gga aga tca gta acc cgc gct caa aca gca gaa aag 48
Met Gly Lys Gly Gly Arg Ser Val Thr Arg Ala Gln Thr Ala Glu Lys
1 5 10 15

tca gca cac acc atc caa acc ttc acc gac ggc cga tgg gtc tcc ccc 96
Ser Ala His Thr Ile Gln Thr Phe Thr Asp Gly Arg Trp Val Ser Pro

20	25	30	
tac aac ccc ctc gca aaa gat gca cct gaa ctc ccc tcc aag ggt gaa Tyr Asn Pro Leu Ala Lys Asp Ala Pro Glu Leu Pro Ser Lys Gly Glu 35 40 45			144
atc aag gcg gtc atc ccc aaa gag tgc ttc gaa cga agc tac ctc cac Ile Lys Ala Val Ile Pro Lys Glu Cys Phe Glu Arg Ser Tyr Leu His 50 55 60			192
tcc atg tac ttc gtc ctc cgt gac acc gtc atg gcc gtg gcc tgc gcc Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala 65 70 75 80			240
tac atc gcc cac tca acg ctc tcc acc gat att ccc tcc gag tta ctg Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu 85 90 95			288
agc gtg gac gca ctc aaa tgg ttc ctc gga tgg aac acc tac gcc ttt Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe 100 105 110			336
tgg atg ggg tgc att ctc acc gga cac tgg gtc cta gcc cat gaa tgt Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys 115 120 125			384
gga cat ggt gca ttc tct ccc tct cag acg ttt aat gac ttt tgg ggg Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly 130 135 140			432
ttc att atg cat cag gcg gtg ttg gtt ccg tat ttc gcc tgg cag tac Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr 145 150 155 160			480
tct cat gcg aag cat cat cga cgt acc aac aac att atg gat ggg gag Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu 165 170 175			528
agc cat gtg ccc aat atc gcc aag gaa atg gga ttg aac gag aag aat Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn 180 185 190			576
gag cgc agt gga gga tat gcc gcc att cat gag gct att gga gat gga Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly 195 200 205			624
ccc ttt gcg atg ttt caa atc ttt gct cac ttg gtg atc ggg tgg cct Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro 210 215 220			672
att tac ttg atg gga ttt gct tcc act gga cgt ctc ggt cag gat ggg Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly 225 230 235 240			720
aag gaa ctt cag gct gga gag atc atc gac cat tac cgt cct tgg agt Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser 245 250 255			768
aag atg ttc ccc acc aag ttg cga ttc aaa att gct ctt tcg aca ctt Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu 260 265 270			816
gga gtg att gcc gcc tgg gtt ggg ttg tac ttt gct gca caa gag tat Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr 275 280 285			864
gga gtc ttg ccc gtg gtt ctt tgg tac att ggc cca ctc atg tgg aat Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn 290 295 300			912

175

290	295	300	
cag gcg tgg ctt gtg ctc tac act tgg ctt cag cac aat gat ccc tcc			960
Gln Ala Trp Leu Val Leu Tyr Thr Trp Leu Gln His Asn Asp Pro Ser			
305	310	315	320
gtg cct caa tat gga agt gac gaa tgg aca tgg gtc aag gga gct ttg			1008
Val Pro Gln Tyr Gly Ser Asp Glu Trp Thr Trp Val Lys Gly Ala Leu			
	325	330	335
tcg acg att gat cgc ccg tat ggt atc ttt gac ttc ttc cat cac aag			1056
Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys			
	340	345	350
att gga agc act cac gta gct cat cat ttg ttc cac gag atg cca ttt			1104
Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe			
	355	360	365
tac aag gcg gat gtg gct act gcg tcg atc aag ggt ttc ttg gag ccg			1152
Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro			
	370	375	380
aag gga ctt tac aac tat gat cca acg cct tgg tat gtg gcc atg tgg			1200
Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp			
	385	390	400
agg gtg gcc aag act tgt cat tat att gag gat gtg gat gga gtt cag			1248
Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln			
	405	410	415
tat tat aag agt ttg gag gat gtg cct ttg aag aag gat gcc aag aag			1296
Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys			
	420	425	430
tct gat tag			1305
Ser Asp			

<210> 110
 <211> 434
 <212> PRT
 <213> Thalassiosira pseudonana

<400> 110

Met Gly Lys Gly Gly Arg Ser Val Thr Arg Ala Gln Thr Ala Glu Lys			
1	5	10	15
Ser Ala His Thr Ile Gln Thr Phe Thr Asp Gly Arg Trp Val Ser Pro			
	20	25	30
Tyr Asn Pro Leu Ala Lys Asp Ala Pro Glu Leu Pro Ser Lys Gly Glu			
	35	40	45
Ile Lys Ala Val Ile Pro Lys Glu Cys Phe Glu Arg Ser Tyr Leu His			
	50	55	60
Ser Met Tyr Phe Val Leu Arg Asp Thr Val Met Ala Val Ala Cys Ala			
65	70	75	80
Tyr Ile Ala His Ser Thr Leu Ser Thr Asp Ile Pro Ser Glu Leu Leu			
	85	90	95

Ser Val Asp Ala Leu Lys Trp Phe Leu Gly Trp Asn Thr Tyr Ala Phe
 100 105 110

Trp Met Gly Cys Ile Leu Thr Gly His Trp Val Leu Ala His Glu Cys
 115 120 125

Gly His Gly Ala Phe Ser Pro Ser Gln Thr Phe Asn Asp Phe Trp Gly
 130 135 140

Phe Ile Met His Gln Ala Val Leu Val Pro Tyr Phe Ala Trp Gln Tyr
 145 150 155 160

Ser His Ala Lys His His Arg Arg Thr Asn Asn Ile Met Asp Gly Glu
 165 170 175

Ser His Val Pro Asn Ile Ala Lys Glu Met Gly Leu Asn Glu Lys Asn
 180 185 190

Glu Arg Ser Gly Gly Tyr Ala Ala Ile His Glu Ala Ile Gly Asp Gly
 195 200 205

Pro Phe Ala Met Phe Gln Ile Phe Ala His Leu Val Ile Gly Trp Pro
 210 215 220

Ile Tyr Leu Met Gly Phe Ala Ser Thr Gly Arg Leu Gly Gln Asp Gly
 225 230 235 240

Lys Glu Leu Gln Ala Gly Glu Ile Ile Asp His Tyr Arg Pro Trp Ser
 245 250 255

Lys Met Phe Pro Thr Lys Leu Arg Phe Lys Ile Ala Leu Ser Thr Leu
 260 265 270

Gly Val Ile Ala Ala Trp Val Gly Leu Tyr Phe Ala Ala Gln Glu Tyr
 275 280 285

Gly Val Leu Pro Val Val Leu Trp Tyr Ile Gly Pro Leu Met Trp Asn
 290 295 300

Gln Ala Trp Leu Val Leu Tyr Thr Trp Leu Gln His Asn Asp Pro Ser
 305 310 315 320

Val Pro Gln Tyr Gly Ser Asp Glu Trp Thr Trp Val Lys Gly Ala Leu
 325 330 335

Ser Thr Ile Asp Arg Pro Tyr Gly Ile Phe Asp Phe Phe His His Lys
 340 345 350

Ile Gly Ser Thr His Val Ala His His Leu Phe His Glu Met Pro Phe
 355 360 365

Tyr Lys Ala Asp Val Ala Thr Ala Ser Ile Lys Gly Phe Leu Glu Pro
370 375 380

Lys Gly Leu Tyr Asn Tyr Asp Pro Thr Pro Trp Tyr Val Ala Met Trp
385 390 395 400

Arg Val Ala Lys Thr Cys His Tyr Ile Glu Asp Val Asp Gly Val Gln
405 410 415

Tyr Tyr Lys Ser Leu Glu Asp Val Pro Leu Lys Lys Asp Ala Lys Lys
420 425 430

Ser Asp

<210> 111
<211> 879
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> CDS
<222> (1)..(879)
<223> Delta-6-Elongase

<400> 111
atg agt ggc tta cgt gca ccc aac ttt tta cac aga ttc tgg aca aag 48
Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
1 5 10 15
tgg gac tac gcg att tcc aaa gtc gtc ttc acg tgt gcc gac agt ttt 96
Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
20 25 30
cag tgg gac atc ggg cca gtg agt tcg agt acg gcg cat tta ccc gcc 144
Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
35 40 45
att gaa tcc cct acc cca ctg gtg act agc ctc ttg ttc tac tta gtc 192
Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Phe Tyr Leu Val
50 55 60
aca gtt ttc ttg tgg tat ggt cgt tta acc agg agt tca gac aag aaa 240
Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
65 70 75 80
att aga gag cct acg tgg tta aga aga ttc ata ata tgt cat aat gcg 288
Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
85 90 95
ttc ttg ata gtc ctc agt ctt tac atg tgc ctt ggt tgt gtg gcc caa 336
Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
100 105 110
gcg tat cag aat gga tat act tta tgg ggt aat gaa ttc aag gcc acg 384
Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
115 120 125
gaa act cag ctt gct ctc tac att tac att ttt tac gta agt aaa ata 432
Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile

178

130	135	140	
tac gag ttt gta gat act	tac att atg ctt ctc aag aat aac ttg cgg		480
Tyr Glu Phe Val Asp Thr	Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg		
145	150	155	160
caa gta agt ttc cta cac att	tat cac cac agc acg att tcc ttt att		528
Gln Val Ser Phe Leu His Ile	Tyr His His Ser Thr Ile Ser Phe Ile		
	165	170	175
tgg tgg atc att gct cgg agg	gct ccg ggt ggt gat gct tac ttc agc		576
Trp Trp Ile Ile Ala Arg Arg	Ala Pro Gly Gly Asp Ala Tyr Phe Ser		
	180	185	190
gcg gcc ttg aac tca tgg gta	cac gtg tgc atg tac acc tat tat cta		624
Ala Ala Leu Asn Ser Trp Val	His Val Cys Met Tyr Thr Tyr Tyr Leu		
	195	200	205
tta tca acc ctt att gga aaa	gaa gat cct aag cgt tcc aac tac ctt		672
Leu Ser Thr Leu Ile Gly Lys	Glu Asp Pro Lys Arg Ser Asn Tyr Leu		
	210	215	220
tgg tgg ggt cgc cac cta acg	caa atg cag atg ctt cag ttt ttc ttc		720
Trp Trp Gly Arg His Leu Thr	Gln Met Gln Met Leu Gln Phe Phe Phe		
	225	230	235
aac gta ctt caa gcg ttg tac	tgc gct tcg ttc tct acg tat ccc aag		768
Asn Val Leu Gln Ala Leu Tyr	Cys Ala Ser Phe Ser Thr Tyr Pro Lys		
	245	250	255
ttt ttg tcc aaa att ctg ctc	gtc tat atg atg agc ctt ctc ggc ttg		816
Phe Leu Ser Lys Ile Leu Leu	Val Tyr Met Met Ser Leu Leu Gly Leu		
	260	265	270
ttt ggg cat ttc tac tat tcc	aag cac ata gca gca gct aag ctc cag		864
Phe Gly His Phe Tyr Tyr Ser	Lys His Ile Ala Ala Ala Lys Leu Gln		
	275	280	285
aaa aaa cag cag tga			879
Lys Lys Gln Gln			
	290		

<210> 112

<211> 292

<212> PRT

<213> *Ostreococcus tauri*

<400> 112

Met Ser Gly Leu Arg Ala Pro Asn Phe Leu His Arg Phe Trp Thr Lys
1 5 10 15

Trp Asp Tyr Ala Ile Ser Lys Val Val Phe Thr Cys Ala Asp Ser Phe
20 25 30

Gln Trp Asp Ile Gly Pro Val Ser Ser Ser Thr Ala His Leu Pro Ala
35 40 45

Ile Glu Ser Pro Thr Pro Leu Val Thr Ser Leu Leu Phe Tyr Leu Val
50 55 60

Thr Val Phe Leu Trp Tyr Gly Arg Leu Thr Arg Ser Ser Asp Lys Lys
65 70 75 80

Ile Arg Glu Pro Thr Trp Leu Arg Arg Phe Ile Ile Cys His Asn Ala
 85 90 95
 Phe Leu Ile Val Leu Ser Leu Tyr Met Cys Leu Gly Cys Val Ala Gln
 100 105 110
 Ala Tyr Gln Asn Gly Tyr Thr Leu Trp Gly Asn Glu Phe Lys Ala Thr
 115 120 125
 Glu Thr Gln Leu Ala Leu Tyr Ile Tyr Ile Phe Tyr Val Ser Lys Ile
 130 135 140
 Tyr Glu Phe Val Asp Thr Tyr Ile Met Leu Leu Lys Asn Asn Leu Arg
 145 150 155 160
 Gln Val Ser Phe Leu His Ile Tyr His His Ser Thr Ile Ser Phe Ile
 165 170 175
 Trp Trp Ile Ile Ala Arg Arg Ala Pro Gly Gly Asp Ala Tyr Phe Ser
 180 185 190
 Ala Ala Leu Asn Ser Trp Val His Val Cys Met Tyr Thr Tyr Tyr Leu
 195 200 205
 Leu Ser Thr Leu Ile Gly Lys Glu Asp Pro Lys Arg Ser Asn Tyr Leu
 210 215 220
 Trp Trp Gly Arg His Leu Thr Gln Met Gln Met Leu Gln Phe Phe Phe
 225 230 235 240
 Asn Val Leu Gln Ala Leu Tyr Cys Ala Ser Phe Ser Thr Tyr Pro Lys
 245 250 255
 Phe Leu Ser Lys Ile Leu Leu Val Tyr Met Met Ser Leu Leu Gly Leu
 260 265 270
 Phe Gly His Phe Tyr Tyr Ser Lys His Ile Ala Ala Ala Lys Leu Gln
 275 280 285
 Lys Lys Gln Gln
 290

<210> 113
 <211> 903
 <212> DNA
 <213> *Ostreococcus tauri*
 <220>
 <221> CDS
 <222> (1)..(903)
 <223> Delta-5-Elongase

<400> 113
 atg agc gcc tcc ggt gcg ctg ctg ccc gcg atc gcg ttc gcc gcg tac 48
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
 1 5 10 15

gcg tac gcg acg tac gcc tac gcc ttt gag tgg tcg cac gcg aat ggc 96
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
 20 25 30

atc gac aac gtc gac gcg cgc gag tgg atc ggt gcg ctg tcg ttg agg 144
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
 35 40 45

ctc ccg gcg atc gcg acg acg atg tac ctg ttg ttc tgc ctg gtc gga 192
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
 50 55 60

ccg agg ttg atg gcg aag cgc gag gcg ttc gac ccg aag ggg ttc atg 240
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
 65 70 75 80

ctg gcg tac aat gcg tat cag acg gcg ttc aac gtc gtc gtg ctc ggg 288
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
 85 90 95

atg ttc gcg cga gag atc tcg ggg ctg ggg cag ccc gtg tgg ggg tca 336
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
 100 105 110

acc atg ccg tgg agc gat aga aaa tcg ttt aag atc ctc ctc ggg gtg 384
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
 115 120 125

tgg ttg cac tac aac aac aaa tat ttg gag cta ttg gac act gtg ttc 432
 Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
 130 135 140

atg gtt gcg cgc aag aag acg aag cag ttg agc ttc ttg cac gtt tat 480
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
 145 150 155 160

cat cac gcc ctg ttg atc tgg gcg tgg tgg ttg gtg tgt cac ttg atg 528
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
 165 170 175

gcc acg aac gat tgt atc gat gcc tac ttc ggc gcg gcg tgc aac tcg 576
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
 180 185 190

ttc att cac atc gtg atg tac tcg tat tat ctc atg tcg gcg ctc ggc 624
 Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
 195 200 205

att cga tgc ccg tgg aag cga tac atc acc cag gct caa atg ctc caa 672
 Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
 210 215 220

ttc gtc att gtc ttc gcg cac gcc gtg ttc gtg ctg cgt cag aag cac 720
 Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
 225 230 235 240

tgc ccg gtc acc ctt cct tgg gcg caa atg ttc gtc atg acg aac atg 768
 Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
 245 250 255

ctc gtg ctc ttc ggg aac ttc tac ctc aag gcg tac tcg aac aag tcg 816
 Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser

181

260 265 270
 cgc ggc gac ggc gcg agt tcc gtg aaa cca gcc gag acc acg cgc gcg 864
 Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
 275 280 285
 ccc agc gtg cga cgc acg cga tct cga aaa att gac taa 903
 Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
 290 295 300
 <210> 114
 <211> 300
 <212> PRT
 <213> *Ostreococcus tauri*
 <400> 114
 Met Ser Ala Ser Gly Ala Leu Leu Pro Ala Ile Ala Phe Ala Ala Tyr
 1 5 10 15
 Ala Tyr Ala Thr Tyr Ala Tyr Ala Phe Glu Trp Ser His Ala Asn Gly
 20 25 30
 Ile Asp Asn Val Asp Ala Arg Glu Trp Ile Gly Ala Leu Ser Leu Arg
 35 40 45
 Leu Pro Ala Ile Ala Thr Thr Met Tyr Leu Leu Phe Cys Leu Val Gly
 50 55 60
 Pro Arg Leu Met Ala Lys Arg Glu Ala Phe Asp Pro Lys Gly Phe Met
 65 70 75 80
 Leu Ala Tyr Asn Ala Tyr Gln Thr Ala Phe Asn Val Val Val Leu Gly
 85 90 95
 Met Phe Ala Arg Glu Ile Ser Gly Leu Gly Gln Pro Val Trp Gly Ser
 100 105 110
 Thr Met Pro Trp Ser Asp Arg Lys Ser Phe Lys Ile Leu Leu Gly Val
 115 120 125
 Trp Leu His Tyr Asn Asn Lys Tyr Leu Glu Leu Leu Asp Thr Val Phe
 130 135 140
 Met Val Ala Arg Lys Lys Thr Lys Gln Leu Ser Phe Leu His Val Tyr
 145 150 155 160
 His His Ala Leu Leu Ile Trp Ala Trp Trp Leu Val Cys His Leu Met
 165 170 175
 Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
 180 185 190
 Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
 195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
290 295 300

<210> 115

<211> 13

<212> PRT

<213> Konsensus

<220>

<221> MISC_FEATURE

<222> (1)..(13)

<223> Xaa in der Sequenz an der Position 2, 3, 4, 6, 7, 8 und 9 hat die
in Tabelle A wiedergegebene Bedeutung.

<400> 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
1 5 10

<210> 116

<211> 10

<212> PRT

<213> Konsensus

<220>

<221> MISC_FEATURE

<222> (1)..(10)

<223> Xaa an der Position 3, 4, 5 und 6 in der Sequenz hat die in Tabel
le A wiedergegebene Bedeutung.

<400> 116

His His Xaa Xaa Xaa Xaa Trp Ala Trp Trp
1 5 10

<210> 117

<211> 909

<212> DNA

<213> Xenopus laevis

<220>

<221> CDS
 <222> (1)..(909)
 <223> Delta-5-Elongase

<400> 117
 atg gcc ttc aag gag ctc aca tca agg gca gtg ctc ctg tat gat gaa 48
 Met Ala Phe Lys Glu Leu Thr Ser Arg Ala Val Leu Leu Tyr Asp Glu
 1 5 10 15
 tgg att aaa gat gct gat cct agg gtt gaa gac tgg cca ctc atg tcc 96
 Trp Ile Lys Asp Ala Asp Pro Arg Val Glu Asp Trp Pro Leu Met Ser
 20 25 30
 tct cct atc cta caa acc atc atc atc ggc gct tac atc tac ttt gtc 144
 Ser Pro Ile Leu Gln Thr Ile Ile Ile Gly Ala Tyr Ile Tyr Phe Val
 35 40 45
 aca tca ttg ggc cca agg atc atg gag aac agg aag ccg ttt gct ctg 192
 Thr Ser Leu Gly Pro Arg Ile Met Glu Asn Arg Lys Pro Phe Ala Leu
 50 55 60
 aag gag atc atg gca tgt tac aac tta ttc atg gtt ctg ttt tct gtg 240
 Lys Glu Ile Met Ala Cys Tyr Asn Leu Phe Met Val Leu Phe Ser Val
 65 70 75 80
 tac atg tgc tat gag ttt ctc atg tcg ggc tgg gct act gga tat tcc 288
 Tyr Met Cys Tyr Glu Phe Leu Met Ser Gly Trp Ala Thr Gly Tyr Ser
 85 90 95
 ttt aga tgt gac att gtt gac tac tct cag tca cct cag gcg tta cgg 336
 Phe Arg Cys Asp Ile Val Asp Tyr Ser Gln Ser Pro Gln Ala Leu Arg
 100 105 110
 atg gcc tgg acc tgc tgg ctc ttc tat ttt tca aag ttc att gaa tta 384
 Met Ala Trp Thr Cys Trp Leu Phe Tyr Phe Ser Lys Phe Ile Glu Leu
 115 120 125
 tta gac act gtt ttc ttt gtg ctg cgt aag aag aac agc cag att aca 432
 Leu Asp Thr Val Phe Phe Val Leu Arg Lys Lys Asn Ser Gln Ile Thr
 130 135 140
 ttc ctg cac gtc tat cac cac tcc att atg cct tgg acg tgg tgg ttt 480
 Phe Leu His Val Tyr His His Ser Ile Met Pro Trp Thr Trp Trp Phe
 145 150 155 160
 gga gtc aaa ttt gct cca ggt ggt ttg ggc aca ttc cat gca ctg gtg 528
 Gly Val Lys Phe Ala Pro Gly Gly Leu Gly Thr Phe His Ala Leu Val
 165 170 175
 aac tgt gtg gtc cat gtt atc atg tac agc tac tac ggc ctg tca gcc 576
 Asn Cys Val Val His Val Ile Met Tyr Ser Tyr Tyr Gly Leu Ser Ala
 180 185 190
 ttg ggg cct gcc tac cag aag tac ctg tgg tgg aaa aag tac atg acg 624
 Leu Gly Pro Ala Tyr Gln Lys Tyr Leu Trp Trp Lys Lys Tyr Met Thr
 195 200 205
 tct atc caa ctg acc cag ttc ttg atg gtt act ttt cac atc ggc cag 672
 Ser Ile Gln Leu Thr Gln Phe Leu Met Val Thr Phe His Ile Gly Gln
 210 215 220
 ttc ttc ttc atg gag aat tgc ccg tac cag tat ccc gtc ttc ttg tat 720
 Phe Phe Phe Met Glu Asn Cys Pro Tyr Gln Tyr Pro Val Phe Leu Tyr
 225 230 235 240
 gtc att tgg ctg tac ggg ttc gtt ttc tta atc ttg ttc ctc aac ttc 768
 Val Ile Trp Leu Tyr Gly Phe Val Phe Leu Ile Leu Phe Leu Asn Phe

184

	245	250	255	
tgg ttc cac gct tac atc aaa gga cag agg ctg ccg aaa gcc gtc caa				816
Trp Phe His Ala Tyr Ile Lys Gly Gln Arg Leu Pro Lys Ala Val Gln				
	260	265	270	
aat ggc cac tgc aag aac aac aac aac caa gaa aac act tgg tgc aag				864
Asn Gly His Cys Lys Asn Asn Asn Asn Gln Glu Asn Thr Trp Cys Lys				
	275	280	285	
aac aaa aac cag aaa aac ggt gca ttg aaa agc aaa aac cat tga				909
Asn Lys Asn Gln Lys Asn Gly Ala Leu Lys Ser Lys Asn His				
	290	295	300	

<210> 118
 <211> 302
 <212> PRT
 <213> *Xenopus laevis*

<400> 118

Met Ala Phe Lys Glu Leu Thr Ser Arg Ala Val Leu Leu Tyr Asp Glu
 1 5 10 15

Trp Ile Lys Asp Ala Asp Pro Arg Val Glu Asp Trp Pro Leu Met Ser
 20 25 30

Ser Pro Ile Leu Gln Thr Ile Ile Ile Gly Ala Tyr Ile Tyr Phe Val
 35 40 45

Thr Ser Leu Gly Pro Arg Ile Met Glu Asn Arg Lys Pro Phe Ala Leu
 50 55 60

Lys Glu Ile Met Ala Cys Tyr Asn Leu Phe Met Val Leu Phe Ser Val
 65 70 75 80

Tyr Met Cys Tyr Glu Phe Leu Met Ser Gly Trp Ala Thr Gly Tyr Ser
 85 90 95

Phe Arg Cys Asp Ile Val Asp Tyr Ser Gln Ser Pro Gln Ala Leu Arg
 100 105 110

Met Ala Trp Thr Cys Trp Leu Phe Tyr Phe Ser Lys Phe Ile Glu Leu
 115 120 125

Leu Asp Thr Val Phe Phe Val Leu Arg Lys Lys Asn Ser Gln Ile Thr
 130 135 140

Phe Leu His Val Tyr His His Ser Ile Met Pro Trp Thr Trp Trp Phe
 145 150 155 160

Gly Val Lys Phe Ala Pro Gly Gly Leu Gly Thr Phe His Ala Leu Val
 165 170 175

Asn Cys Val Val His Val Ile Met Tyr Ser Tyr Tyr Gly Leu Ser Ala
 180 185 190

185

Leu Gly Pro Ala Tyr Gln Lys Tyr Leu Trp Trp Lys Lys Tyr Met Thr
 195 200 205

Ser Ile Gln Leu Thr Gln Phe Leu Met Val Thr Phe His Ile Gly Gln
 210 215 220

Phe Phe Phe Met Glu Asn Cys Pro Tyr Gln Tyr Pro Val Phe Leu Tyr
 225 230 235 240

Val Ile Trp Leu Tyr Gly Phe Val Phe Leu Ile Leu Phe Leu Asn Phe
 245 250 255

Trp Phe His Ala Tyr Ile Lys Gly Gln Arg Leu Pro Lys Ala Val Gln
 260 265 270

Asn Gly His Cys Lys Asn Asn Asn Asn Gln Glu Asn Thr Trp Cys Lys
 275 280 285

Asn Lys Asn Gln Lys Asn Gly Ala Leu Lys Ser Lys Asn His
 290 295 300

<210> 119
 <211> 870
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(870)
 <223> Delta-5-Elongase

<400> 119
 atg gac gta ctt cat cgt ttc tta gga ttc tac gaa tgg acg ctg act 48
 Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr
 1 5 10 15
 ttc gcg gac ccc cga gtg gca aaa tgg cct tta ata gaa aac ccc ctt 96
 Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu
 20 25 30
 cct aca att gct att gtg ttg ctg tac ctg gcg ttt gtt ctg tat att 144
 Pro Thr Ile Ala Ile Val Leu Leu Tyr Leu Ala Phe Val Leu Tyr Ile
 35 40 45
 ggg ccg cgt ttt atg cga aaa aga gca cca gtt gac ttt ggt tta ttc 192
 Gly Pro Arg Phe Met Arg Lys Arg Ala Pro Val Asp Phe Gly Leu Phe
 50 55 60
 ctc cct gga tat aac ttt gct ttg gtt gca tta aat tat tat atc ctg 240
 Leu Pro Gly Tyr Asn Phe Ala Leu Val Ala Leu Asn Tyr Tyr Ile Leu
 65 70 75 80
 caa gaa gtg gtc act ggg agt tat ggg gct ggg tat gat ttg gtt tgc 288
 Gln Glu Val Val Thr Gly Ser Tyr Gly Ala Gly Tyr Asp Leu Val Cys
 85 90 95
 aca cca ctt cga agt gat tcc tac gat ccc aat gaa atg aag gtt gca 336
 Thr Pro Leu Arg Ser Asp Ser Tyr Asp Pro Asn Glu Met Lys Val Ala

186

100	105	110	
aac gct gta tgg tgg tat tat	gta tcc aag ata ata	gag ttg ttt gat	384
Asn Ala Val Trp Trp Tyr Tyr	Val Ser Lys Ile Ile	Glu Leu Phe Asp	
115	120	125	
act gtg ttg ttc act cta cgc	aaa cga gac cga caa gta act ttc ctt		432
Thr Val Leu Phe Thr Leu Arg	Lys Arg Asp Arg Gln Val Thr Phe Leu		
130	135	140	
cat gtt tat cac cat tct acc atg ccc ctg ttg tgg tgg att ggg gca			480
His Val Tyr His His Ser Thr Met Pro Leu Leu Trp Trp Ile Gly Ala			
145	150	155	160
aag tgg gtg cct ggt ggg caa tca ttt gtt ggc atc ata ctg aac tcc			528
Lys Trp Val Pro Gly Gly Gln Ser Phe Val Gly Ile Ile Leu Asn Ser			
165	170	175	
agt gtt cat gtt atc atg tat acg tac tat gga ttg tca gcc ttg ggg			576
Ser Val His Val Ile Met Tyr Thr Tyr Tyr Gly Leu Ser Ala Leu Gly			
180	185	190	
cct cac atg cag aag ttt cta tgg tgg aag aaa tat atc aca atg ttg			624
Pro His Met Gln Lys Phe Leu Trp Trp Lys Lys Tyr Ile Thr Met Leu			
195	200	205	
caa ctg gtt caa ttt gtt ctt gcc atc tac cat act gct cga tca ttg			672
Gln Leu Val Gln Phe Val Leu Ala Ile Tyr His Thr Ala Arg Ser Leu			
210	215	220	
tac gtt aaa tgt ccc tcg cct gtt tgg atg cac tgg gca ctt atc ttg			720
Tyr Val Lys Cys Pro Ser Pro Val Trp Met His Trp Ala Leu Ile Leu			
225	230	235	240
tac gct ttc tca ttc att ttg ctt ttc tca aac ttc tac atg cat gcc			768
Tyr Ala Phe Ser Phe Ile Leu Leu Phe Ser Asn Phe Tyr Met His Ala			
245	250	255	
tat atc aag aaa tca aga aaa ggg aaa gag aat ggc agt cga gga aaa			816
Tyr Ile Lys Lys Ser Arg Lys Gly Lys Glu Asn Gly Ser Arg Gly Lys			
260	265	270	
ggt ggt gta agt aat gga aag gaa aag ctg cac gct aat ggt aaa acc			864
Gly Gly Val Ser Asn Gly Lys Glu Lys Leu His Ala Asn Gly Lys Thr			
275	280	285	
gat taa			870
Asp			

<210> 120

<211> 289

<212> PRT

<213> Ciona intestinalis

<400> 120

Met Asp Val Leu His Arg Phe Leu Gly Phe Tyr Glu Trp Thr Leu Thr
1 5 10 15

Phe Ala Asp Pro Arg Val Ala Lys Trp Pro Leu Ile Glu Asn Pro Leu
20 25 30

Pro Thr Ile Ala Ile Val Leu Leu Tyr Leu Ala Phe Val Leu Tyr Ile
35 40 45

Gly Pro Arg Phe Met Arg Lys Arg Ala Pro Val Asp Phe Gly Leu Phe
 50 55 60

Leu Pro Gly Tyr Asn Phe Ala Leu Val Ala Leu Asn Tyr Tyr Ile Leu
 65 70 75 80

Gln Glu Val Val Thr Gly Ser Tyr Gly Ala Gly Tyr Asp Leu Val Cys
 85 90 95

Thr Pro Leu Arg Ser Asp Ser Tyr Asp Pro Asn Glu Met Lys Val Ala
 100 105 110

Asn Ala Val Trp Trp Tyr Tyr Val Ser Lys Ile Ile Glu Leu Phe Asp
 115 120 125

Thr Val Leu Phe Thr Leu Arg Lys Arg Asp Arg Gln Val Thr Phe Leu
 130 135 140

His Val Tyr His His Ser Thr Met Pro Leu Leu Trp Trp Ile Gly Ala
 145 150 155 160

Lys Trp Val Pro Gly Gly Gln Ser Phe Val Gly Ile Ile Leu Asn Ser
 165 170 175

Ser Val His Val Ile Met Tyr Thr Tyr Tyr Gly Leu Ser Ala Leu Gly
 180 185 190

Pro His Met Gln Lys Phe Leu Trp Trp Lys Lys Tyr Ile Thr Met Leu
 195 200 205

Gln Leu Val Gln Phe Val Leu Ala Ile Tyr His Thr Ala Arg Ser Leu
 210 215 220

Tyr Val Lys Cys Pro Ser Pro Val Trp Met His Trp Ala Leu Ile Leu
 225 230 235 240

Tyr Ala Phe Ser Phe Ile Leu Leu Phe Ser Asn Phe Tyr Met His Ala
 245 250 255

Tyr Ile Lys Lys Ser Arg Lys Gly Lys Glu Asn Gly Ser Arg Gly Lys
 260 265 270

Gly Gly Val Ser Asn Gly Lys Glu Lys Leu His Ala Asn Gly Lys Thr
 275 280 285

Asp

<210> 121

<211> 30

<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223>

<400> 121
aggatccatg gccttcaagg agctcacatc

30

<210> 122
<211> 35
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(35)
<223>

<400> 122
cctcgagtca atgggttttg cttttcaatg caccg

35

<210> 123
<211> 25
<212> DNA
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<220>
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<222> (1)..(25)
<223>

<400> 123
taagcttatg gacgtacttc atcgt

25

<210> 124
<211> 26
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(26)
<223>

<400> 124
tcagatcttt aatcggtttt accatt

26

<210> 125
<211> 34
<212> DNA
<213> Primer

<220>
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<222> (1)..(34)
<223>

<400> 125
gcggccgcac catggccttc aaggagctca catc 34

<210> 126
<211> 38
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(38)
<223>

<400> 126
gcggccgcct tcaatggttt ttgcttttca atgcacgg 38

<210> 127
<211> 29
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(29)
<223>

<400> 127
gcggccgcac catggacgta cttcatcgt 29

<210> 128
<211> 27
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223>

<400> 128
gcggccgctt taatcggttt taccatt 27

<210> 129
<211> 60
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(60)
<223>

<400> 129
gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> 130
<211> 60
<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(60)

<223>

<400> 130

gtcgaccgcg gcactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> 131

<211> 789

<212> DNA

<213> Euglena gracilis

<220>

<221> CDS

<222> (1)..(789)

<223> Delta-5-Elongase

<400> 131

atg	ctg	ggg	gcc	atc	gcg	gac	gtc	gtg	ctc	cgg	ggg	ccc	gcc	gca	ttc	48
Met	Leu	Gly	Ala	Ile	Ala	Asp	Val	Val	Leu	Arg	Gly	Pro	Ala	Ala	Phe	
1				5					10					15		

cac	tgg	gac	cct	gcc	acc	acc	ccg	ctc	gca	tcg	atc	gtc	agc	ccc	tgt	96
His	Trp	Asp	Pro	Ala	Thr	Thr	Pro	Leu	Ala	Ser	Ile	Val	Ser	Pro	Cys	
			20					25					30			

gtg	gcc	tcc	gtg	gcg	tac	ctg	ggg	gcc	atc	ggg	ctg	ctg	aag	cgc	cgc	144
Val	Ala	Ser	Val	Ala	Tyr	Leu	Gly	Ala	Ile	Gly	Leu	Leu	Lys	Arg	Arg	
		35					40					45				

act	gga	ccg	gag	gtc	cgc	tcc	aag	ccc	ttc	gag	ctg	cta	cac	aac	ggg	192
Thr	Gly	Pro	Glu	Val	Arg	Ser	Lys	Pro	Phe	Glu	Leu	Leu	His	Asn	Gly	
	50					55					60					

ctg	ctg	gtg	ggc	tgg	tcc	ctc	gtg	gtg	ctg	ctc	ggg	acg	ctg	tac	ggc	240
Leu	Leu	Val	Gly	Trp	Ser	Leu	Val	Val	Leu	Leu	Gly	Thr	Leu	Tyr	Gly	
65					70				75					80		

gcg	ttc	cag	cgc	gtg	cag	gag	gac	ggc	cgg	ggg	gtg	cag	gcc	ctc	ctg	288
Ala	Phe	Gln	Arg	Val	Gln	Glu	Asp	Gly	Arg	Gly	Val	Gln	Ala	Leu	Leu	
			85					90						95		

tgc	acc	cag	cgg	cca	cca	tct	cag	atc	tgg	gac	ggc	ccg	gtg	ggg	tac	336
Cys	Thr	Gln	Arg	Pro	Pro	Ser	Gln	Ile	Trp	Asp	Gly	Pro	Val	Gly	Tyr	
			100					105					110			

ttc	acg	tac	ctc	ttc	tac	ctc	gcg	aag	tac	tgg	gag	ctg	gcg	gac	act	384
Phe	Thr	Tyr	Leu	Phe	Tyr	Leu	Ala	Lys	Tyr	Trp	Glu	Leu	Ala	Asp	Thr	
		115				120						125				

gtc	atc	ctc	gcc	ctc	cgc	cag	aag	ccc	acc	atc	ccc	ctc	cac	gtc	tac	432
Val	Ile	Leu	Ala	Leu	Arg	Gln	Lys	Pro	Thr	Ile	Pro	Leu	His	Val	Tyr	
	130					135					140					

cat	cac	gcc	gtc	atg	ctg	ttc	atc	gtg	tgg	tcg	tgg	ttc	gcg	cac	ccc	480
His	His	Ala	Val	Met	Leu	Phe	Ile	Val	Trp	Ser	Trp	Phe	Ala	His	Pro	
145					150					155					160	

tgg	ctc	gag	ggg	agc	tgg	tgg	tgc	tcc	ctg	gtc	aac	tct	ttc	atc	cac	528
Trp	Leu	Glu	Gly	Ser	Trp	Trp	Cys	Ser	Leu	Val	Asn	Ser	Phe	Ile	His	
				165					170					175		

191

acg gtg atg tac tcg tac tac acc ctg acg gtg gtt ggc atc aac cct 576
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro
 180 185 190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg 624
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr
 195 200 205

ggc tgc gtg tac gtc atg gcg ttc ttc ggc cta tat tat gcc ggg gcg 672
 Gly Cys Val Tyr Val Met Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala
 210 215 220

ggc tgc acc tcc aac gtg tac act gcc tgg ttc tcg atg ggg gtc aac 720
 Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn
 225 230 235 240

ctc agc ttt ctg tgg ctc ttc gct ctt ttc ttc cgc cgg tca tac agc 768
 Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser
 245 250 255

aaa cct agc cgg aag gag tag 789
 Lys Pro Ser Arg Lys Glu
 260

<210> 132
 <211> 262
 <212> PRT
 <213> Euglena gracilis

<400> 132

Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe
 1 5 10 15

His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys
 20 25 30

Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg
 35 40 45

Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly
 50 55 60

Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly
 65 70 75 80

Ala Phe Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu
 85 90 95

Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr
 100 105 110

Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Ala Asp Thr
 115 120 125

Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr
 130 135 140

192

His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro
145 150 155 160

Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His
165 170 175

Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro
180 185 190

Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr
195 200 205

Gly Cys Val Tyr Val Met Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala
210 215 220

Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn
225 230 235 240

Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser
245 250 255

Lys Pro Ser Arg Lys Glu
260

<210> 133
<211> 789
<212> DNA
<213> Euglena gracilis

<220>
<221> CDS
<222> (1)..(789)
<223> Delta-5-Elongase

<400> 133
atg ctg ggg gcc atc gcg gac gtc gtg ctc cgg ggg ccc gcc gca ttc 48
Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe
1 5 10 15

cac tgg gac cct gcc acc acc ccg ctc gca tcg atc gtc agc ccc tgt 96
His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys
20 25 30

gtg gcc tcc gtg gcg tac ctg ggg gcc atc ggg ctg ctg aag cgc cgc 144
Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg
35 40 45

act gga ccg gag gtc cgc tcc aag ccc ttc gag ctg cta cac aac ggg 192
Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly
50 55 60

ctg ctg gtg ggc tgg tcc ctc gtg gtg ctg ctc ggg acg ctg tac ggc 240
Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly
65 70 75 80

gcg tac cag cgc gtg cag gag gac ggc cgg ggg gtg cag gcc ctg ctg 288
Ala Tyr Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu
85 90 95

193

tgc acc cag cgg cca cca tct cag atc tgg gac ggc ccg gtg ggg tac 336
 Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr
 100 105 110

ttc acg tac ctt ttc tac ctc gcg aag tac tgg gag ctg gtg gac act 384
 Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Val Asp Thr
 115 120 125

gtc atc ctc gcc ctc cgc cag aag ccc acc atc ccc ctc cac gtc tac 432
 Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr
 130 135 140

cat cac gcc gtc atg ctg ttc att gtg tgg tgc tcc ctg gtc aac tct ttc atc cac 480
 His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro
 145 150 155 160

tgg ctc gag ggg agc tgg tgg tgc tcc ctg gtc aac tct ttc atc cac 528
 Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His
 165 170 175

acg gtg atg tac tgc tat tac acc ctg acg gtg gtt ggc atc aac cct 576
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro
 180 185 190

tgg tgg aag aag tgg atg acc acc atg cag atc atc cag ttc atc acg 624
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr
 195 200 205

ggc tgc gtg tac gtc acg gcg ttc ttc ggc cta tac tat gcc ggg gcg 672
 Gly Cys Val Tyr Val Thr Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala
 210 215 220

ggc tgc acc tcc aac gtg tac act gcc tgg ttc tgc atg ggg gtc aac 720
 Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn
 225 230 235 240

ctc agc ttt ctg tgg ctc ttc gct ctt ttc ttc cgc cgg tgc tac agc 768
 Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser
 245 250 255

aaa cct agc cgg aag gag tag 789
 Lys Pro Ser Arg Lys Glu
 260

<210> 134
 <211> 262
 <212> PRT
 <213> Euglena gracilis

<400> 134

Met Leu Gly Ala Ile Ala Asp Val Val Leu Arg Gly Pro Ala Ala Phe
 1 5 10 15

His Trp Asp Pro Ala Thr Thr Pro Leu Ala Ser Ile Val Ser Pro Cys
 20 25 30

Val Ala Ser Val Ala Tyr Leu Gly Ala Ile Gly Leu Leu Lys Arg Arg
 35 40 45

Thr Gly Pro Glu Val Arg Ser Lys Pro Phe Glu Leu Leu His Asn Gly
 50 55 60

194

Leu Leu Val Gly Trp Ser Leu Val Val Leu Leu Gly Thr Leu Tyr Gly
 65 70 75 80
 Ala Tyr Gln Arg Val Gln Glu Asp Gly Arg Gly Val Gln Ala Leu Leu
 85 90 95
 Cys Thr Gln Arg Pro Pro Ser Gln Ile Trp Asp Gly Pro Val Gly Tyr
 100 105 110
 Phe Thr Tyr Leu Phe Tyr Leu Ala Lys Tyr Trp Glu Leu Val Asp Thr
 115 120 125
 Val Ile Leu Ala Leu Arg Gln Lys Pro Thr Ile Pro Leu His Val Tyr
 130 135 140
 His His Ala Val Met Leu Phe Ile Val Trp Ser Trp Phe Ala His Pro
 145 150 155 160
 Trp Leu Glu Gly Ser Trp Trp Cys Ser Leu Val Asn Ser Phe Ile His
 165 170 175
 Thr Val Met Tyr Ser Tyr Tyr Thr Leu Thr Val Val Gly Ile Asn Pro
 180 185 190
 Trp Trp Lys Lys Trp Met Thr Thr Met Gln Ile Ile Gln Phe Ile Thr
 195 200 205
 Gly Cys Val Tyr Val Thr Ala Phe Phe Gly Leu Tyr Tyr Ala Gly Ala
 210 215 220
 Gly Cys Thr Ser Asn Val Tyr Thr Ala Trp Phe Ser Met Gly Val Asn
 225 230 235 240
 Leu Ser Phe Leu Trp Leu Phe Ala Leu Phe Phe Arg Arg Ser Tyr Ser
 245 250 255
 Lys Pro Ser Arg Lys Glu
 260

<210> 135
 <211> 897
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(897)
 <223> Delta-5-Elongase

<400> 135
 atg gca tct gtt tac tcc acc cta acc tac tgg ctc gtc cac cac ccc
 Met Ala Ser Val Tyr Ser Thr Leu Thr Tyr Trp Leu Val His His Pro
 1 5 10 15

195

tac att gcc aac ttc acg tgg acc gaa ggt gaa aca cta ggc tcc acc Tyr Ile Ala Asn Phe Thr Trp Thr Glu Gly Glu Thr Leu Gly Ser Thr 20 25 30	96
gtt ttc ttt gtc ttt gtc gtc gtc tcc ctt tac ctc tcc gcc aca ttc Val Phe Phe Val Phe Val Val Val Ser Leu Tyr Leu Ser Ala Thr Phe 35 40 45	144
ctc ctc cga tac acc gtc gat tca ctc ccc aca ctc ggt ccc cgc att Leu Leu Arg Tyr Thr Val Asp Ser Leu Pro Thr Leu Gly Pro Arg Ile 50 55 60	192
ctc aaa cca atc aca gcc gtt cac agc ctc att ctc ttc ctc ctc tcc Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Phe Leu Leu Ser 65 70 75 80	240
tta acc atg gcc gtt ggt tgc act ctc tcc cta atc tct tcc tcg gac Leu Thr Met Ala Val Gly Cys Thr Leu Ser Leu Ile Ser Ser Ser Asp 85 90 95	288
ccg aag gcg cgt ctc ttc gac gcc gtt tgt ttc ccc ctc gac gtg aaa Pro Lys Ala Arg Leu Phe Asp Ala Val Cys Phe Pro Leu Asp Val Lys 100 105 110	336
cct aag gga ccg ctt ttc ttt tgg gct caa gtc ttt tac ctc tcg aag Pro Lys Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr Leu Ser Lys 115 120 125	384
atc ctt gag ttc gta gac aca ctt ctc atc ata ctc aac aaa tca atc Ile Leu Glu Phe Val Asp Thr Leu Leu Ile Ile Leu Asn Lys Ser Ile 130 135 140	432
caa cgg ctc tcg ttc ctc cac gtc tac cac cac gca acg gtt gtg att Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr Val Val Ile 145 150 155 160	480
ttg tgc tac ctc tgg tta cga aca cgt caa tcg atg ttt cct gtt ggg Leu Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe Pro Val Gly 165 170 175	528
ctc gtg ttg aac tcg acg gtc cat gtg att atg tac ggg tac tat ttc Leu Val Leu Asn Ser Thr Val His Val Ile Met Tyr Gly Tyr Tyr Phe 180 185 190	576
ctc tgc gct atc gga tcg agg ccc aag tgg aag aag ttg gtg acg aat Leu Cys Ala Ile Gly Ser Arg Pro Lys Trp Lys Lys Leu Val Thr Asn 195 200 205	624
ttt caa atg gtt cag ttt gct ttc ggc atg ggg tta gga gcc gct tgg Phe Gln Met Val Gln Phe Ala Phe Gly Met Gly Leu Gly Ala Ala Trp 210 215 220	672
atg ctc cca gag cat tat ttc ggg tcg ggt tgc gcc ggg att tgg aca Met Leu Pro Glu His Tyr Phe Gly Ser Gly Cys Ala Gly Ile Trp Thr 225 230 235 240	720
gtt tat ttc aat ggt gtg ttt act gct tct cta ttg gct ctc ttc tac Val Tyr Phe Asn Gly Val Phe Thr Ala Ser Leu Leu Ala Leu Phe Tyr 245 250 255	768
aac ttc cac tcc aag aac tat gag aag act aca acg tcg cct ttg tat Asn Phe His Ser Lys Asn Tyr Glu Lys Thr Thr Thr Ser Pro Leu Tyr 260 265 270	816
aag atc gaa tcc ttt ata ttt att cac gga gag agg tgg gca aat aaa Lys Ile Glu Ser Phe Ile Phe Ile His Gly Glu Arg Trp Ala Asn Lys 275 280 285	864

196

897

gcg att aca tta ttt tcc aag aaa aac gat taa
 Ala Ile Thr Leu Phe Ser Lys Lys Asn Asp
 290 295

<210> 136
 <211> 298
 <212> PRT
 <213> Arabidopsis thaliana

<400> 136

Met Ala Ser Val Tyr Ser Thr Leu Thr Tyr Trp Leu Val His His Pro
 1 5 10 15

Tyr Ile Ala Asn Phe Thr Trp Thr Glu Gly Glu Thr Leu Gly Ser Thr
 20 25 30

Val Phe Phe Val Phe Val Val Val Ser Leu Tyr Leu Ser Ala Thr Phe
 35 40 45

Leu Leu Arg Tyr Thr Val Asp Ser Leu Pro Thr Leu Gly Pro Arg Ile
 50 55 60

Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Phe Leu Leu Ser
 65 70 75 80

Leu Thr Met Ala Val Gly Cys Thr Leu Ser Leu Ile Ser Ser Ser Asp
 85 90 95

Pro Lys Ala Arg Leu Phe Asp Ala Val Cys Phe Pro Leu Asp Val Lys
 100 105 110

Pro Lys Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr Leu Ser Lys
 115 120 125

Ile Leu Glu Phe Val Asp Thr Leu Leu Ile Ile Leu Asn Lys Ser Ile
 130 135 140

Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr Val Val Ile
 145 150 155 160

Leu Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe Pro Val Gly
 165 170 175

Leu Val Leu Asn Ser Thr Val His Val Ile Met Tyr Gly Tyr Tyr Phe
 180 185 190

Leu Cys Ala Ile Gly Ser Arg Pro Lys Trp Lys Lys Leu Val Thr Asn
 195 200 205

Phe Gln Met Val Gln Phe Ala Phe Gly Met Gly Leu Gly Ala Ala Trp
 210 215 220

197

Met Leu Pro Glu His Tyr Phe Gly Ser Gly Cys Ala Gly Ile Trp Thr
 225 230 235 240

Val Tyr Phe Asn Gly Val Phe Thr Ala Ser Leu Leu Ala Leu Phe Tyr
 245 250 255

Asn Phe His Ser Lys Asn Tyr Glu Lys Thr Thr Thr Ser Pro Leu Tyr
 260 265 270

Lys Ile Glu Ser Phe Ile Phe Ile His Gly Glu Arg Trp Ala Asn Lys
 275 280 285

Ala Ile Thr Leu Phe Ser Lys Lys Asn Asp
 290 295

<210> 137
 <211> 837
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(837)
 <223> Delta-5-Elongase

<400> 137
 atg gca tca att tac tcc tct tta acc tac tgg ctc gtt aac cac ccc 48
 Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro
 1 5 10 15
 tac atc tcc aat ttt act tgg atc gaa ggt gaa acc cta ggc tcc acc 96
 Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr
 20 25 30
 gtc ttt ttc gta tcc gtc gta gtc tcc gtt tac ctc tcc gcc acg ttc 144
 Val Phe Phe Val Ser Val Val Val Ser Val Tyr Leu Ser Ala Thr Phe
 35 40 45
 ctc ctc cga tcc gcc atc gat tca gtc cca tca ctc agt cca cgt atc 192
 Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile
 50 55 60
 ctc aaa ccg atc aca gcc gtc cac agc cta atc ctc tgt ctc ctc tcc 240
 Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser
 65 70 75 80
 tta gtc atg gcc gtc ggt tgc act ctc tca ata acc tca tct cac gcg 288
 Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala
 85 90 95
 tct tca gat ccg atg gcg cgt ttc ctt cac gcg att tgc ttt ccc gtc 336
 Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val
 100 105 110
 gac gtt aaa cct aac gga ccg ctt ttc ttc tgg gct caa gtc ttc tac 384
 Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr
 115 120 125
 ctc tcg aag atc ctc gag ttc gga gac acg atc ctc atc ata ctc ggc 432
 Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly
 130 135 140

198

aaa tca atc caa cgg cta tcc ttc ctc cac gtg tac cac cac gcg acg 480
 Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr
 145 150 155 160

 gtt gtg gtc atg tgt tat ctc tgg ctc cga act cgc caa tcg atg ttt 528
 Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe
 165 170 175

 ccg att gcg ctc gtg acg aat tcg acg gta cac gtc atc atg tac ggt 576
 Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly
 180 185 190

 tac tac ttc ctc tgc gcc gtt gga tcg agg ccc aag tgg aag aga ttg 624
 Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu
 195 200 205

 gtg acg gat tgt cag att gtt cag ttt gtt ttc agt ttc ggg tta tcc 672
 Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser
 210 215 220

 ggt tgg atg ctc cga gag cac tta ttc ggg tcg ggt tgc acc ggg att 720
 Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile
 225 230 235 240

 tgg gga tgg tgt ttc aac gct gca ttt aat gct tct ctt ttg gct ctc 768
 Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu
 245 250 255

 ttt tcc aac ttc cat tca aag aat tat gtc aag aag cca acg aga gag 816
 Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu
 260 265 270

 gat ggc aaa aaa agc gat tag 837
 Asp Gly Lys Lys Ser Asp
 275

<210> 138
 <211> 278
 <212> PRT
 <213> Arabidopsis thaliana

<400> 138

Met Ala Ser Ile Tyr Ser Ser Leu Thr Tyr Trp Leu Val Asn His Pro
 1 5 10 15

 Tyr Ile Ser Asn Phe Thr Trp Ile Glu Gly Glu Thr Leu Gly Ser Thr
 20 25 30

 Val Phe Phe Val Ser Val Val Val Ser Val Tyr Leu Ser Ala Thr Phe
 35 40 45

 Leu Leu Arg Ser Ala Ile Asp Ser Leu Pro Ser Leu Ser Pro Arg Ile
 50 55 60

 Leu Lys Pro Ile Thr Ala Val His Ser Leu Ile Leu Cys Leu Leu Ser
 65 70 75 80

 Leu Val Met Ala Val Gly Cys Thr Leu Ser Ile Thr Ser Ser His Ala
 85 90 95

199

Ser Ser Asp Pro Met Ala Arg Phe Leu His Ala Ile Cys Phe Pro Val
 100 105 110

Asp Val Lys Pro Asn Gly Pro Leu Phe Phe Trp Ala Gln Val Phe Tyr
 115 120 125

Leu Ser Lys Ile Leu Glu Phe Gly Asp Thr Ile Leu Ile Ile Leu Gly
 130 135 140

Lys Ser Ile Gln Arg Leu Ser Phe Leu His Val Tyr His His Ala Thr
 145 150 155 160

Val Val Val Met Cys Tyr Leu Trp Leu Arg Thr Arg Gln Ser Met Phe
 165 170 175

Pro Ile Ala Leu Val Thr Asn Ser Thr Val His Val Ile Met Tyr Gly
 180 185 190

Tyr Tyr Phe Leu Cys Ala Val Gly Ser Arg Pro Lys Trp Lys Arg Leu
 195 200 205

Val Thr Asp Cys Gln Ile Val Gln Phe Val Phe Ser Phe Gly Leu Ser
 210 215 220

Gly Trp Met Leu Arg Glu His Leu Phe Gly Ser Gly Cys Thr Gly Ile
 225 230 235 240

Trp Gly Trp Cys Phe Asn Ala Ala Phe Asn Ala Ser Leu Leu Ala Leu
 245 250 255

Phe Ser Asn Phe His Ser Lys Asn Tyr Val Lys Lys Pro Thr Arg Glu
 260 265 270

Asp Gly Lys Lys Ser Asp
 275

<210> 139

<211> 6

<212> PRT

<213> Konsensus

<220>

<221> MISC_FEATURE

<222> (1)..(6)

<223> Xaa in der Position 3 und 4 in der Sequenz hat die in Tabelle A w
 iedergegebene Bedeutung.

<400> 139

Leu His Xaa Xaa His His
 1 5

<210> 140

<211> 8

<212> PRT
<213> Konsensus

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> Xaa an der Position 2, 3, 5 und 6 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 140

Thr Xaa Xaa Gln Xaa Xaa Gln Phe
1 5

<210> 141
<211> 6
<212> PRT
<213> Konsensus

<220>
<221> MISC_FEATURE
<222> (1)..(6)
<223> Xaa an Position 3 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 141

Asp Thr Xaa Phe Met Val
1 5

<210> 142
<211> 8
<212> PRT
<213> Konsensus

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> Xaa an Position 5 und 6 in der Sequenz hat die in Tabelle A wiedergegebene Bedeutung.

<400> 142

Thr Gln Ala Gln Xaa Xaa Gln Phe
1 5

<210> 143
<211> 60
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(60)
<223>

<400> 143
gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> 144

201

<211> 60
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(60)
<223>

<400> 144
gtcgaccgcg gcactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa 60

<210> 145
<211> 36
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(36)
<223>

<400> 145
ggtaccacat aatgtgcgtg gagacggaaa ataacg 36

<210> 146
<211> 33
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(33)
<223>

<400> 146
ctcgagttac gccgtctttc cggagtgttg gcc 33

<210> 147
<211> 24
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(24)
<223>

<400> 147
gcggccgctt acgtggactt ggtc 24

<210> 148
<211> 24
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(24)
<223>

<400> 148
gcggccgcat ggcgacgaag gagg

24

<210> 149
<211> 25
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(25)
<223>

<400> 149
taagcttaca tggcgacgaa ggagg

25

<210> 150
<211> 24
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(24)
<223>

<400> 150
tggatccact tacgtggact tgggt

24

<210> 151
<211> 60
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(60)
<223>

<400> 151
gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 152
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223>

<400> 152
gcggccgcac catgtgctca ccaccgccgt c

31

<210> 153
<211> 26

<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(26)
<223>

<400> 153
gcggccgcct acatggcacc agtaac

26

<210> 154
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223>

<400> 154
gcggccgcac catgtgctca tcaccgccgt c

31

<210> 155
<211> 26
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(26)
<223>

<400> 155
gcggccgcct acatggcacc agtaac

26

<210> 156
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223>

<400> 156
gcggccgcac catggacgcc tacaacgctg c

31

<210> 157
<211> 27
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223>

<400> 157
gcggcgcct aagcactctt cttcttt

27

<210> 158
<211> 23
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(23)
<223>

<400> 158
accatgtgct caccaccgcc gtc

23

<210> 159
<211> 18
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(18)
<223>

<400> 159
ctacatggca ccagtaac

18

<210> 160
<211> 23
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(23)
<223>

<400> 160
accatgtgct catcaccgcc gtc

23

<210> 161
<211> 18
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(18)
<223>

<400> 161
ctacatggca ccagtaac

18

<210> 162
<211> 23
<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(23)

<223>

<400> 162

accatggacg cctacaacgc tgc

23

<210> 163

<211> 19

<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(19)

<223>

<400> 163

ctaagcactc ttcttcttt

19

<210> 164

<211> 60

<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(60)

<223>

<400> 164

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 165

<211> 60

<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(60)

<223>

<400> 165

gtcgacccgc ggactagtgg gccctctaga cccgggggat ccggatctgc tggctatgaa

60

<210> 166

<211> 29

<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(29)

<223>

<400> 166
gcggccgcat aatgacgagc aacatgagc

29

<210> 167
<211> 29
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(29)
<223>

<400> 167
gcggccgctt aggccgactt ggccttggg

29

<210> 168
<211> 34
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(34)
<223>

<400> 168
gcggccgcac catggacgtc gtcgagcagc aatg

34

<210> 169
<211> 36
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(36)
<223>

<400> 169
gcggccgctt agatgggtctt ctgcttcttg ggcgcc

36

<210> 170
<211> 23
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(23)
<223>

<400> 170
gacataatga cgagcaacat gag

23

<210> 171
<211> 25
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(25)
<223>

<400> 171
cggccttaggc cgacttggcc ttggg

25

<210> 172
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223>

<400> 172
agacataatg gacgtcgtcg agcagcaatg

30

<210> 173
<211> 28
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(28)
<223>

<400> 173
ttagatgggc ttctgcttct tgggcgcc

28

<210> 174
<211> 60
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(60)
<223>

<400> 174
gtcgaccgc ggactagtgg gccctctaga cccgggggat ccgatctgc tggctatgaa

60

<210> 175
<211> 29
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(29)
<223>

<400> 175

gcggccgcat aatggcttca acatggcaa

29

<210> 176
<211> 32
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(32)
<223>

<400> 176
gcggccgctt atgtcttctt gctcttcctg tt

32

<210> 177
<211> 26
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(26)
<223>

<400> 177
gcggccgcat aatggagact tttaat

26

<210> 178
<211> 28
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(28)
<223>

<400> 178
gcggccgctc agtccccct cactttcc

28

<210> 179
<211> 29
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(29)
<223>

<400> 179
aagcttacat aatggcttca acatggcaa

29

<210> 180
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223>

<400> 180
ggatccttat gtcttcttgc tcttctgtt

30

<210> 181
<211> 26
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(26)
<223>

<400> 181
aagcttacat aatggagact tttaat

26

<210> 182
<211> 27
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223>

<400> 182
ggatccttca gtccccctc actttcc

27

<210> 183
<211> 993
<212> DNA
<213> Phaeodactylum tricornutum

<220>
<221> CDS
<222> (103)..(939)
<223> Delta-6-Elongase

<400> 183
ggtcttttgt ggtagctatc gtcacacac gcaggctcgtt gctcactatc gtgatccgta
tattgaccgt gcacttgtgt aaaacagaga tattttcaaga gt atg atg gta cct
Met Met Val Pro
1

60

114

tca agt tat gac gag tat atc gtc atg gtc aac gac ctt ggc gac tct
Ser Ser Tyr Asp Glu Tyr Ile Val Met Val Asn Asp Leu Gly Asp Ser
5 10 15 20

162

att ctg agc tgg gcc gac cct gat cac tat cgt gga cat acc gag gga
Ile Leu Ser Trp Ala Asp Pro Asp His Tyr Arg Gly His Thr Glu Gly
25 30 35

210

tgg gag ttc act gac ttt tct gct gct ttt agc att gcc gtc gcg tac
Trp Glu Phe Thr Asp Phe Ser Ala Ala Phe Ser Ile Ala Val Ala Tyr

258

210

40	45	50	
ctc ctg ttt gtc ttt gtt gga tct ctc att atg agt atg gga gtc ccc Leu Leu Phe Val Phe Val Gly Ser Leu Ile Met Ser Met Gly Val Pro 55 60 65			306
gca att gac cct tat ccg ctc aag ttt gtc tac aat gtt tca cag att Ala Ile Asp Pro Tyr Pro Leu Lys Phe Val Tyr Asn Val Ser Gln Ile 70 75 80			354
atg ctt tgt gct tac atg acc att gaa gcc agt ctt cta gct tat cgt Met Leu Cys Ala Tyr Met Thr Ile Glu Ala Ser Leu Leu Ala Tyr Arg 85 90 95 100			402
aac ggc tac aca ttc tgg cct tgc aac gat tgg gac ttt gaa aag ccg Asn Gly Tyr Thr Phe Trp Pro Cys Asn Asp Trp Asp Phe Glu Lys Pro 105 110 115			450
cct atc gct aag ctc ctc tgg ctc ttt tac gtt tcc aaa att tgg gat Pro Ile Ala Lys Leu Leu Trp Leu Phe Tyr Val Ser Lys Ile Trp Asp 120 125 130			498
ttt tgg gac acc atc ttt att gtt ctc ggg aag aag tgg cgt caa ctt Phe Trp Asp Thr Ile Phe Ile Val Leu Gly Lys Lys Trp Arg Gln Leu 135 140 145			546
tcc ttc ctg cac gtc tac cat cac acc acc atc ttt ctc ttc tac tgg Ser Phe Leu His Val Tyr His His Thr Thr Ile Phe Leu Phe Tyr Trp 150 155 160			594
ttg aat gca cat gta aac ttt gat ggt gat att ttc ctc acc atc gtc Leu Asn Ala His Val Asn Phe Asp Gly Asp Ile Phe Leu Thr Ile Val 165 170 175 180			642
ttg aac ggt ttc atc cac acc gtc atg tac acg tac tac ttc att tgc Leu Asn Gly Phe Ile His Thr Val Met Tyr Thr Tyr Tyr Phe Ile Cys 185 190 195			690
atg cac acc aag gtc cca gag acc ggc aaa tcc ttg ccc att tgg tgg Met His Thr Lys Val Pro Glu Thr Gly Lys Ser Leu Pro Ile Trp Trp 200 205 210			738
aaa tct agt ttg aca agc atg cag ctg gtg cag ttc atc acg atg atg Lys Ser Ser Leu Thr Ser Met Gln Leu Val Gln Phe Ile Thr Met Met 215 220 225			786
acg cag gct atc atg atc ttg tac aag ggc tgt gct gct ccc cat agc Thr Gln Ala Ile Met Ile Leu Tyr Lys Gly Cys Ala Ala Pro His Ser 230 235 240			834
cgg gtg gtg aca tcg tac ttg gtt tac att ttg tcg ctc ttt att ttg Arg Val Val Thr Ser Tyr Leu Val Tyr Ile Leu Ser Leu Phe Ile Leu 245 250 255 260			882
ttc gcc cag ttc ttt gtc agc tca tac ctc aag ccg aag aag aag aag Phe Ala Gln Phe Phe Val Ser Ser Tyr Leu Lys Pro Lys Lys Lys Lys 265 270 275			930
aca gct taa gcgaaatttg ggtctacgtt aaaacaatta cgttacaaaa Thr Ala			979
aaaaaaaaaa aaaa			993

<210> 184

<211> 278

<212> PRT

211

<213> Phaeodactylum tricornutum

<400> 184

Met Met Val Pro Ser Ser Tyr Asp Glu Tyr Ile Val Met Val Asn Asp
 1 5 10 15

Leu Gly Asp Ser Ile Leu Ser Trp Ala Asp Pro Asp His Tyr Arg Gly
 20 25 30

His Thr Glu Gly Trp Glu Phe Thr Asp Phe Ser Ala Ala Phe Ser Ile
 35 40 45

Ala Val Ala Tyr Leu Leu Phe Val Phe Val Gly Ser Leu Ile Met Ser
 50 55 60

Met Gly Val Pro Ala Ile Asp Pro Tyr Pro Leu Lys Phe Val Tyr Asn
 65 70 75 80

Val Ser Gln Ile Met Leu Cys Ala Tyr Met Thr Ile Glu Ala Ser Leu
 85 90 95

Leu Ala Tyr Arg Asn Gly Tyr Thr Phe Trp Pro Cys Asn Asp Trp Asp
 100 105 110

Phe Glu Lys Pro Pro Ile Ala Lys Leu Leu Trp Leu Phe Tyr Val Ser
 115 120 125

Lys Ile Trp Asp Phe Trp Asp Thr Ile Phe Ile Val Leu Gly Lys Lys
 130 135 140

Trp Arg Gln Leu Ser Phe Leu His Val Tyr His His Thr Thr Ile Phe
 145 150 155 160

Leu Phe Tyr Trp Leu Asn Ala His Val Asn Phe Asp Gly Asp Ile Phe
 165 170 175

Leu Thr Ile Val Leu Asn Gly Phe Ile His Thr Val Met Tyr Thr Tyr
 180 185 190

Tyr Phe Ile Cys Met His Thr Lys Val Pro Glu Thr Gly Lys Ser Leu
 195 200 205

Pro Ile Trp Trp Lys Ser Ser Leu Thr Ser Met Gln Leu Val Gln Phe
 210 215 220

Ile Thr Met Met Thr Gln Ala Ile Met Ile Leu Tyr Lys Gly Cys Ala
 225 230 235 240

Ala Pro His Ser Arg Val Val Thr Ser Tyr Leu Val Tyr Ile Leu Ser
 245 250 255

212

Leu Phe Ile Leu Phe Ala Gln Phe Phe Val Ser Ser Tyr Leu Lys Pro
 260 265 270

Lys Lys Lys Lys Thr Ala
 275

<210> 185
 <211> 20
 <212> DNA
 <213> Primer

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> N in den Positionen 3 und 18 bedeutet C oder T.

<400> 185
 aaactuctut ggctuttnta

20

<210> 186
 <211> 23
 <212> DNA
 <213> Primer

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> N in den Positionen 3 und 15 bedeutet C oder T. N in den Positionen 9, 12 und 21 bedeutet A oder G.

<400> 186
 gantguacna anaantgugc naa

23

<210> 187
 <211> 446
 <212> DNA
 <213> PCR-Fragment

<220>
 <221> misc_feature
 <222> (1)..(446)
 <223> PCR-Fragment

<400> 187
 aagctcctct ggctctttta cgtttccaaa atttgggatt tttgggacac catctttatt 60
 gttctcggga agaagtggcg tcaactttcc ttctgcacg tctaccatca caccaccatc 120
 tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt cctcaccatc 180
 gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg catgcacacc 240
 aagggtcccag agaccggcaa atccttgccc atttgggtgga aatctagtgt gacaagcatg 300
 cagctgggtgc agttcatcac gatgatgacg caggctatca tgatcttgta caagggtgt 360
 gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc gctctttatt 420
 ttgttcgccc agttctttgt cagctc 446

213

<210> 188
<211> 30
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(30)
<223>

<400> 188
gcggccgcac ataatgatgg taccttcaag

30

<210> 189
<211> 22
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(22)
<223>

<400> 189
gaagacagct taatagacta gt

22

<210> 190
<211> 31
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(31)
<223>

<400> 190
gcggccgcac catgatggta ccttcaagtt a

31

<210> 191
<211> 24
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (1)..(24)
<223>

<400> 191
gaagacagct taataggcgg ccgc

24

<210> 192
<211> 859
<212> DNA
<213> PCR-Produkt

<400> 192
gcggccgcac ataatgatgg taccttcaag ttatgacgag tatatcgtca tgggtcaacga

60

214

ccttggecgac tctattctga gctggggccga ccctgatcac tatcgtggac ataccgaggg	120
atgggagttc actgactttt ctgctgcttt tagcattgcc gtcgcgtacc tcctgtttgt	180
ctttgttgga tctctcatta tgagtatggg agtccccgca attgaccctt atccgctcaa	240
gtttgtctac aatgtttcac agattatgct ttgtgcttac atgaccattg aagccagtct	300
tctagcttat cgtaacggct acacattctg gccttgcaac gattgggact ttgaaaagcc	360
gcctatcgct aagctcctct ggctctttta cgtttccaaa atttgggatt tttgggacac	420
catctttatt gttctcggga agaagtggcg tcaactttcc ttctgcacg tctaccatca	480
caccaccatc tttctcttct actggttgaa tgcacatgta aactttgatg gtgatatttt	540
cctcaccatc gtcttgaacg gtttcatcca caccgtcatg tacacgtact acttcatttg	600
catgcacacc aaggtcccag agaccggcaa atccttgccc atttgggtgga aatctagttt	660
gacaaycatg cagctgggtgc agttcatcac gatgatgacg caggctatca tgatcttgta	720
caagggctgt gctgctcccc atagccgggt ggtgacatcg tacttggttt acattttgtc	780
gctctttatt ttgttcgccc agttctttgt cagctcatac ctcaagccga agaagaagaa	840
gacagcttaa tagactagt	859

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